SEQUENCE LISTING

09/673133

<400> 1

```
atgaaacaca ttcctttaac cacactgtgt gtggcaatct ctgccgtctt attaaccgct 60
tgtggtggca gtggtggttc aaatccacct gctcctacgc ccattccaaa tgctagcggt 120
tcaggtaata ctggcaacac tggtaatgct ggcggtactg ataatacagc caatgcaggt 180
aatacaggcg gtacaaactc tggtacaggc agtgccaaca caccagaacc aaaatataaa 240
gatgtgccaa ccgatgaaaa taaaaaagat gaagtgtcag gcattcaaga acctgccatg 300
ggttatggca tggctttgag taaaatgaat ctacacaaac aacaagacac gccattagat 360
gaaaaagata tcattacctt agacggtaaa aaacaagttg caaaaggtga aaaatcgcca 420
ttgccatttt cgttggatgt agaaaataaa ttgcttgatg ctatatagc aaaaatgaat 480
gaagcggata aaaatgccat tggtgacaga attaagaaag ataataaaga caagtcatta 540
tctaaagcag agcttgccaa acaaatcaaa gaagatgtgc gtaaaagcca tgagtttcag 600
caagtattat catcactgaa aaacaaaatt tttcattcaa atgatggaac aaccaaagca 660
accacacgag atttacaata tgttgattat ggttactact tggtgaatga tggcaattat 720
ctaaccgtca aaacagacga actttggaat ttaggccctg tgggcggtgt gtttttataat 780
ggcacaacga ccgccaaaga gctacccaca caagatgcgg tcaaatataa aggacattgg 840
gactttatga ccgatgttgc caaacaaaga aaccgattta gcgaagtgaa agaaaacctt 900
caagcaggtc ggtattatgg agcatcttca aaagatgaat acaaccgctt attaactgat 960
gagaaaaaca aaccagagcg ttataacggt gaatatggtc atagcagtga gtttactgtt 1020
aattttaagg acaaaaaatt aacaggtgag ctgtttagta acctacaaga cagccgtaag 1080
ggcaatgtta cgaaaaccaa acgctatgac atcgatgcca atatctacgg caaccgcttc 1140
cgtggcagtg ccaccgcaag cgataaagca gaagcaagca aaaccaaaca cccctttacc 1200
agcgatgcca aaaatagcct agaaggcggt ttttatggac caaacgccga ggagctggca 1260
ggtaaattcc taaccaatga caacaaactc tttggcgtct ttggtgctaa acgagagagt 1320
aaagctgggg aaaaaaccga agccatctta gatgcctatg cacttgggac atttaacaaa 1380
aataacgcaa ccacattcac cccatttacc aaaaaacaac tggataactt ggcaatgcc 1440
aaaaagttgg tcttgggttc taccgtcatt gatttggtgc ctaccggtgt caccaaagat 1500
gtcaatgaat tcaccaaaaa caagccagat tctgccacaa acaaagcggg cgagactttg 1560
```

```
atggtgaatg ataaagttag cgtcaaaacc tatggctatg cagaaactt tgaatacccta 1620
aaatttggtg agctcagtgt cggcacaagc aacagcgtct ttttacaagg cgaacgcacc 1680
gctaccacag gcgagaaagc cgtaccaacc aaaggcacag ccaaatattt ggggaactgg 1740
gtaggataca tcacaggaaa ggactcatca aaaagcttta atgaggccca agatgttgct 1800
gattttgaca ttgactttga gaaaaaatca gttaaaggca aactgaccac caaagaccgc 1860
caagaccctg tatttaacat cacaggtgac atcgcaggca atggctggac aggcaaagcc 1920
agcaccacca aagcggacgc agggggctac aagatagatt ctagcagtac aggcaaatcc 1980
atcgtcatca agatgccga ggttacaggg ggctttttatg gtccaaatgc aaacgagatg 2040
ggcgggtcat ttacacacaa caccgatgac agtaaagcct ctgtggtctt tggcacaaaa 2100
agacaagaag aagttaagta g                                            2121
```

<210> 2
<211> 706
<212> PRT
<213> Moraxella catarrhalis

<400> 2

```
Met Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val
  1               5                  10                  15

Leu Leu Thr Ala Cys Gly Gly Ser Gly Gly Ser Asn Pro Pro Ala Pro
               20                  25                  30

Thr Pro Ile Pro Asn Ala Ser Gly Ser Gly Asn Thr Gly Asn Thr Gly
           35                  40                  45

Asn Ala Gly Gly Thr Asp Asn Thr Ala Asn Ala Gly Asn Thr Gly Gly
       50                  55                  60

Thr Asn Ser Gly Thr Gly Ser Ala Asn Thr Pro Glu Pro Lys Tyr Lys
 65                  70                  75                  80

Asp Val Pro Thr Asp Glu Asn Lys Lys Asp Glu Val Ser Gly Ile Gln
               85                  90                  95

Glu Pro Ala Met Gly Tyr Gly Met Ala Leu Ser Lys Met Asn Leu His
              100                 105                 110

Lys Gln Gln Asp Thr Pro Leu Asp Glu Lys Asp Ile Ile Thr Leu Asp
           115                 120                 125

Gly Lys Lys Gln Val Ala Lys Gly Glu Lys Ser Pro Leu Pro Phe Ser
           130                 135                 140

Leu Asp Val Glu Asn Lys Leu Leu Asp Gly Tyr Ile Ala Lys Met Asn
145                 150                 155                 160

Glu Ala Asp Lys Asn Ala Ile Gly Asp Arg Ile Lys Lys Asp Asn Lys
                165                 170                 175

Asp Lys Ser Leu Ser Lys Ala Glu Leu Ala Lys Gln Ile Lys Glu Asp
               180                 185                 190

Val Arg Lys Ser His Glu Phe Gln Gln Val Leu Ser Ser Leu Lys Asn
           195                 200                 205

Lys Ile Phe His Ser Asn Asp Gly Thr Thr Lys Ala Thr Thr Arg Asp
           210                 215                 220
```

```
Leu Gln Tyr Val Asp Tyr Gly Tyr Tyr Leu Val Asn Asp Gly Asn Tyr
225             230              235           240

Leu Thr Val Lys Thr Asp Glu Leu Trp Asn Leu Gly Pro Val Gly Gly
            245              250              255

Val Phe Tyr Asn Gly Thr Thr Thr Ala Lys Glu Leu Pro Thr Gln Asp
            260              265              270

Ala Val Lys Tyr Lys Gly His Trp Asp Phe Met Thr Asp Val Ala Lys
            275              280              285

Gln Arg Asn Arg Phe Ser Glu Val Lys Glu Asn Leu Gln Ala Gly Arg
    290              295              300

Tyr Tyr Gly Ala Ser Ser Lys Asp Glu Tyr Asn Arg Leu Leu Thr Asp
305              310              315              320

Glu Lys Asn Lys Pro Glu Arg Tyr Asn Gly Glu Tyr Gly His Ser Ser
            325              330              335

Glu Phe Thr Val Asn Phe Lys Asp Lys Lys Leu Thr Gly Glu Leu Phe
            340              345              350

Ser Asn Leu Gln Asp Ser Arg Lys Gly Asn Val Thr Lys Thr Lys Arg
    355              360              365

Tyr Asp Ile Asp Ala Asn Ile Tyr Gly Asn Arg Phe Arg Gly Ser Ala
    370              375              380

Thr Ala Ser Asp Lys Ala Glu Ala Ser Lys Thr Lys His Pro Phe Thr
385              390              395              400

Ser Asp Ala Lys Asn Ser Leu Glu Gly Gly Phe Tyr Gly Pro Asn Ala
            405              410              415

Glu Glu Leu Ala Gly Lys Phe Leu Thr Asn Asp Asn Lys Leu Phe Gly
            420              425              430

Val Phe Gly Ala Lys Arg Glu Ser Lys Ala Gly Glu Lys Thr Glu Ala
            435              440              445

Ile Leu Asp Ala Tyr Ala Leu Gly Thr Phe Asn Lys Asn Asn Ala Thr
    450              455              460

Thr Phe Thr Pro Phe Thr Lys Lys Gln Leu Asp Asn Phe Gly Asn Ala
465              470              475              480

Lys Lys Leu Val Leu Gly Ser Thr Val Ile Asp Leu Val Pro Thr Gly
            485              490              495

Val Thr Lys Asp Val Asn Glu Phe Thr Lys Asn Lys Pro Asp Ser Ala
            500              505              510

Thr Asn Lys Ala Gly Glu Thr Leu Met Val Asn Asp Lys Val Ser Val
            515              520              525
```

```
Lys Thr Tyr Gly Tyr Gly Arg Asn Phe Glu Tyr Leu Lys Phe Gly Glu
    530                 535                 540

Leu Ser Val Gly Thr Ser Asn Ser Val Phe Leu Gln Gly Glu Arg Thr
545                 550                 555                 560

Ala Thr Thr Gly Glu Lys Ala Val Pro Thr Lys Gly Thr Ala Lys Tyr
                565                 570                 575

Leu Gly Asn Trp Val Gly Tyr Ile Thr Gly Lys Asp Ser Ser Lys Ser
                580                 585                 590

Phe Asn Glu Ala Gln Asp Val Ala Asp Phe Asp Ile Asp Phe Glu Lys
        595                 600                 605

Lys Ser Val Lys Gly Lys Leu Thr Thr Lys Asp Arg Gln Asp Pro Val
    610                 615                 620

Phe Asn Ile Thr Gly Asp Ile Ala Gly Asn Gly Trp Thr Gly Lys Ala
625                 630                 635                 640

Ser Thr Thr Lys Ala Asp Ala Gly Gly Tyr Lys Ile Asp Ser Ser Ser
                645                 650                 655

Thr Gly Lys Ser Ile Val Ile Lys Asp Ala Glu Val Thr Gly Gly Phe
                660                 665                 670

Tyr Gly Pro Asn Ala Asn Glu Met Gly Gly Ser Phe Thr His Asn Thr
        675                 680                 685

Asp Asp Ser Lys Ala Ser Val Val Phe Gly Thr Lys Arg Gln Glu Glu
    690                 695                 700

Val Lys
705
```

```
<210> 3
<211> 2139
<212> DNA
<213> Moraxella catarrhalis

<400> 3
atgaaacaca ttcctttaac cacactgtgt gtggcaatct ctgccgtctt attaaccgct   60
tgtggtggca gtggtggttc aaatccacct gctcctacgc ccattccaaa tgcaggcggt  120
gcaggtaatg ctggtagcgg tactggcggt gcaggtagca ctgataatgc agccaatgca  180
ggcagtacag gcggtgcaag ctctggtaca ggcagtgcca gcacacaaaa accaaaatat  240
caagatgtgc caaccgataa aaataaaaaa gatgaagtgt caggcattca agaacctgcc  300
atgggttatg gcgtggaatt aaagcttcgt aactggatac cacaagaaca ggaagaacat  360
gccaaaatca atacaaatga tgttgtaaaa cttgaaggtg acttgaagca taatccattt  420
gacaactcta tttggcaaaa catcaaaaat agcaaagaag tacaaactgt ttacaaccaa  480
gagaagcaaa acattgaaaa tcaaatcaaa aaagaaaata agaacttga taaaacggca  540
ctaaaagctc ttattgaaaa agttcttgat gactatctaa caagtcttgc taaacccatt  600
tatgaaaaaa atattaatga ttcacatgat aagcagaata agcacgcac tcgtgatttg  660
aagtatgtgc gttctggtta tatttatcgc tcaggttatt ctaatatcga cattcaaaag  720
aaaatagcta aaactggttt tgatggtgct ttattttata aaggtacaca aactgctaaa  780
caattgcctg tatctgaggt taagtataaa ggcacttggg attttatgac cgatgccaaa  840
aaaggacaat catttagcag ttttgaaaga cgagctggtg atcgctatag tgcaatgtct  900
```

```
tcccatgagt acccatcttt attaactgat gataaaaaca aaccagataa ttataacgat 960
gaatatggtc atagcagtga gtttacggta gattttagta aaaagagcct aacaggtggg 1020
ctgtttagta acctacaaga ccaccataag ggcaaggtta cgaaaaccaa acgctatgac 1080
atcaatgccc gtatccacgg taaccgcttc cgtggcagtg ccaccgcaat caataaagat 1140
aatgaaagca aagccaaaca ccccctttacc agcgatgccg acaataggct agaaggcggt 1200
ttttatggac caaacgccga ggagctggca ggtaaattcc taaccgatga caacaaactc 1260
tttggtgtct ttggtgctaa acaagagagt gaagctaagg aaaccgaagc catcttagat 1320
gcttatgcac ttgggacatt taataaatct ggtacgacca atcctgcctt taccgccaat 1380
agtaaaaaag aactggataa ctttggcaat attaataaat tggtcttggg ttctactgtg 1440
atagacctta ctcaaggtaa tgattttgta aaaaccattg ataaagaaaa gccagccacc 1500
actaccaatc aagcaggcga gcctttgacg gtgaatgata aggttcgggt acaagtttgt 1560
tgtagcaatc ttgagcatct aaaatttggc tcactgagta tcggtgatag taatagcgtc 1620
tttttacaag gtgaacgcac cgctaccaaa ggtgataaag ataaagccat gccagttgca 1680
ggaaatgcta ataccgtgg tacatgggca ggctatgttg caggctctgg caataccagc 1740
aaagcctatg aagcccaaca atttgctgac aatgccaacc gtgccgagtt tgatgtagac 1800
tttgctaaca aaagcctaac tggtaagctt attccaaata cgagcagtga tggtaaatct 1860
gcttttgata ttactgctac aattgatggc aatggtttta gtggtaaagc caatacacca 1920
gatattgaaa caggtgggtt aaagattgac agtaagaaca gtgaaagcgg ccgagtaatt 1980
gtgaaagatg ctatagttat aggtggcttt tatggtccac aagctaatga actgggtggc 2040
tcatttacct acaagagcaa tgatgctgga aatcaagaca aagacagtag tgcatctgtg 2100
gtctttggtg caagaaaaca acaagaagtc aaaccatga              2139
```

<210> 4
<211> 712
<212> PRT
<213> Moraxella catarrhalis

<400> 4

```
Met Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val
  1               5                  10                  15

Leu Leu Thr Ala Cys Gly Gly Ser Gly Gly Ser Asn Pro Pro Ala Pro
             20                  25                  30

Thr Pro Ile Pro Asn Ala Gly Gly Ala Gly Asn Ala Gly Ser Gly Thr
         35                  40                  45

Gly Gly Ala Gly Ser Thr Asp Asn Ala Ala Asn Ala Gly Ser Thr Gly
     50                  55                  60

Gly Ala Ser Ser Gly Thr Gly Ser Ala Ser Thr Gln Lys Pro Lys Tyr
 65                  70                  75                  80

Gln Asp Val Pro Thr Asp Lys Asn Lys Lys Asp Glu Val Ser Gly Ile
                 85                  90                  95

Gln Glu Pro Ala Met Gly Tyr Gly Val Glu Leu Lys Leu Arg Asn Trp
            100                 105                 110

Ile Pro Gln Glu Gln Glu Glu His Ala Lys Ile Asn Thr Asn Asp Val
            115                 120                 125

Val Lys Leu Glu Gly Asp Leu Lys His Asn Pro Phe Asp Asn Ser Ile
        130                 135                 140

Trp Gln Asn Ile Lys Asn Ser Lys Glu Val Gln Thr Val Tyr Asn Gln
145                 150                 155                 160
```

Glu Lys Gln Asn Ile Glu Asn Gln Ile Lys Lys Glu Asn Lys Glu Leu
            165   170   175

Asp Lys Thr Ala Leu Lys Ala Leu Ile Glu Lys Val Leu Asp Asp Tyr
            180   185   190

Leu Thr Ser Leu Ala Lys Pro Ile Tyr Glu Lys Asn Ile Asn Asp Ser
            195   200   205

His Asp Lys Gln Asn Lys Ala Arg Thr Arg Asp Leu Lys Tyr Val Arg
    210   215   220

Ser Gly Tyr Ile Tyr Arg Ser Gly Tyr Ser Asn Ile Asp Ile Gln Lys
225   230   235   240

Lys Ile Ala Lys Thr Gly Phe Asp Gly Ala Leu Phe Tyr Lys Gly Thr
            245   250   255

Gln Thr Ala Lys Gln Leu Pro Val Ser Glu Val Lys Tyr Lys Gly Thr
            260   265   270

Trp Asp Phe Met Thr Asp Ala Lys Lys Gly Gln Ser Phe Ser Ser Phe
            275   280   285

Glu Arg Arg Ala Gly Asp Arg Tyr Ser Ala Met Ser Ser His Glu Tyr
    290   295   300

Pro Ser Leu Leu Thr Asp Asp Lys Asn Lys Pro Asp Asn Tyr Asn Asp
305   310   315   320

Glu Tyr Gly His Ser Ser Glu Phe Thr Val Asp Phe Ser Lys Lys Ser
            325   330   335

Leu Thr Gly Gly Leu Phe Ser Asn Leu Gln Asp His His Lys Gly Lys
            340   345   350

Val Thr Lys Thr Lys Arg Tyr Asp Ile Asn Ala Arg Ile His Gly Asn
            355   360   365

Arg Phe Arg Gly Ser Ala Thr Ala Ile Asn Lys Asp Asn Glu Ser Lys
    370   375   380

Ala Lys His Pro Phe Thr Ser Asp Ala Asp Asn Arg Leu Glu Gly Gly
385   390   395   400

Phe Tyr Gly Pro Asn Ala Glu Glu Leu Ala Gly Lys Phe Leu Thr Asp
            405   410   415

Asp Asn Lys Leu Phe Gly Val Phe Gly Ala Lys Gln Glu Ser Glu Ala
            420   425   430

Lys Glu Thr Glu Ala Ile Leu Asp Ala Tyr Ala Leu Gly Thr Phe Asn
            435   440   445

Lys Ser Gly Thr Thr Asn Pro Ala Phe Thr Ala Asn Ser Lys Lys Glu
            450   455   460

Leu Asp Asn Phe Gly Asn Ile Asn Lys Leu Val Leu Gly Ser Thr Val
465   470   475   480

```
Ile Asp Leu Thr Gln Gly Asn Asp Phe Val Lys Thr Ile Asp Lys Glu
             485             490             495

Lys Pro Ala Thr Thr Thr Asn Gln Ala Gly Glu Pro Leu Thr Val Asn
             500             505             510

Asp Lys Val Arg Val Gln Val Cys Cys Ser Asn Leu Glu His Leu Lys
             515             520             525

Phe Gly Ser Leu Ser Ile Gly Asp Ser Asn Ser Val Phe Leu Gln Gly
     530             535             540

Glu Arg Thr Ala Thr Lys Gly Asp Lys Asp Lys Ala Met Pro Val Ala
545             550             555             560

Gly Asn Ala Lys Tyr Arg Gly Thr Trp Ala Gly Tyr Val Ala Gly Ser
             565             570             575

Gly Asn Thr Ser Lys Ala Tyr Glu Ala Gln Gln Phe Ala Asp Asn Ala
             580             585             590

Asn Arg Ala Glu Phe Asp Val Asp Phe Ala Asn Lys Ser Leu Thr Gly
     595             600             605

Lys Leu Ile Pro Asn Thr Ser Ser Asp Gly Lys Ser Ala Phe Asp Ile
     610             615             620

Thr Ala Thr Ile Asp Gly Asn Gly Phe Ser Gly Lys Ala Asn Thr Pro
625             630             635             640

Asp Ile Glu Thr Gly Gly Leu Lys Ile Asp Ser Lys Asn Ser Glu Ser
             645             650             655

Gly Arg Val Ile Val Lys Asp Ala Ile Val Ile Gly Gly Phe Tyr Gly
             660             665             670

Pro Gln Ala Asn Glu Leu Gly Gly Ser Phe Thr Tyr Lys Ser Asn Asp
     675             680             685

Ala Gly Asn Gln Asp Lys Asp Ser Ser Ala Ser Val Val Phe Gly Ala
     690             695             700

Arg Lys Gln Gln Glu Val Lys Pro
705             710


<210> 5
<211> 2142
<212> DNA
<213> Moraxella catarrhalis

<400> 5
atgaaacaca ttcctttaac cacactgtgt gtggcaatct ctgccgtctt attaaccgct    60
tgtggtggca gtggtggttc aaatccacct gctcctacgc ccatcccaaa tgcaggcagt   120
gcaggtaatg ctggcggtac aggaaataca ggcggtactg cagtactga taatgtaggc   180
aatgctggcg gtgcaaactc tggtacaggc aatgcaggta attcaggtaa tgcaaactct   240
ggtacaggca gtgccaacac accagaacca aaatatcaag atgtgccaac cgataaaaat   300
gaaaaagaac aagtttcatc cattcaagaa cctgccatgg gttatgcaat ggaattaaag   360
```

```
cttcgtaatg ctcaccctct taacccaaat aaaaataaag aggctgaaaa acgcattgcc 420
ttagaccaaa aagatttggt ggcagtagag ggcgacctaa ccaacattcc ttttgataaa 480
aatcttattg aataccttaa aaaatcatcc gaggttgtaa gtaaatttga agcacaaaaa 540
ggcggtattg aaaataacac aagactgaca cacaaagatt tatcatcaga gcaaaaagaa 600
gcaaaagtca aagaagcgtt ggacaatgct ttaactcaat ttgcccaaga aaaatacaag 660
gagctaattg agaacgccca tgataaaaaa tctgacgcac gcaaccgtga tctagaatat 720
gtcaagtctg gttttaacta tctttctgga tataccgcca ccgaccacga caaaaaaacc 780
aattatcgtg gctattatgg tgcgttgtat tataaaggca gcgaaaccgc caaagagcta 840
ccacaaacaa gtgcaaaata taaaggttat tgggacttta tgacagatgc cacacttgat 900
aacaaataca cggatttgcc aggtatcgcc agacaaaccc agtggcgtag tcttgtttct 960
actgatgagt atgcaacgct cttgacagac aaaaataaca agcccagtga ttacaatggt 1020
gcatatggtc atagcagtga atttgatgtt aattttgctg ataaaaaaat taaaggcaaa 1080
cttatcagta atcagttatc aggcacagct gtaaccgcca aagagcgtta taaaatagaa 1140
gctgatatcc acggcaaccg cttccgtggc agtgccaccg caagcgataa agcagaagac 1200
agcaaaaccc aacacccctt taccagcgat gctacaaaca agctagaagg tggtttttat 1260
ggaccaaaag gcgaggagct ggcaggtaaa ttcttaaccg atgacaacaa actctttggg 1320
gtctttggtg ctaaacgaga taaagtagaa aaaaccgaag ccatcttaga tgcctatgca 1380
cttgggacat ttaataatac aaataaagca accacattca ccccatttac caaaaaacaa 1440
ctggataact ttggcaatgc caaaaagttg gtcttgggtt ctaccgtcat taatttggtg 1500
tctaccgatg ccaccaaaaa tgaattcacc aaaaaattca ccaaagacaa gccaacttct 1560
gccacaaaca aagcgggcga ctttgatg gtgaatgatg aagttatcgt caaaacctat 1620
ggcaaaaact ttgaatacct aaaatttggt gagcttagtg tcggtgatag ccatagcgtc 1680
tttttacaag gcgaacgcac cgctaccaca ggcgagaaag ccgtaccaac cacaggcaaa 1740
gccaaatatc tggggaactg ggtaggatac atcacaggag cgggcacagg aaaaagcttt 1800
aatgaggccc aagatattgc tgattttgac attgactttg agagaaaatc agttaaaggc 1860
aaactgacca cccaaggccg cacagatcct gtctttaaca tcaaaggtga aattgcaggc 1920
aatggctgga caggcaaagc cagcaccacc aaagcggacg caggaggcta caagatagat 1980
tctagcagta caggcaaatc catcgtcatc gaaaatgccg aagttactgg gggcttttat 2040
ggtccaaatg caaacgagat gggcgggtca tttacacacg ataccgatga cagtaaagcc 2100
tctgtggtct ttggcacaaa aagacaacaa gaagttaagt ag 2142
```

```
<210> 6
<211> 713
<212> PRT
<213> Moraxella catarrhalis

<400> 6
Met Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val
  1               5                  10                  15

Leu Leu Thr Ala Cys Gly Gly Ser Gly Gly Ser Asn Pro Pro Ala Pro
            20                  25                  30

Thr Pro Ile Pro Asn Ala Gly Ser Ala Gly Asn Ala Gly Gly Thr Gly
        35                  40                  45

Asn Thr Gly Gly Thr Gly Ser Thr Asp Asn Val Gly Asn Ala Gly Gly
    50                  55                  60

Ala Asn Ser Gly Thr Gly Asn Ala Gly Asn Ser Gly Asn Ala Asn Ser
65                  70                  75                  80

Gly Thr Gly Ser Ala Asn Thr Pro Glu Pro Lys Tyr Gln Asp Val Pro
                85                  90                  95

Thr Asp Lys Asn Glu Lys Glu Gln Val Ser Ser Ile Gln Glu Pro Ala
            100                 105                 110
```

Met Gly Tyr Ala Met Glu Leu Lys Leu Arg Asn Ala His Pro Leu Asn
    115   120   125

Pro Asn Lys Asn Lys Glu Ala Glu Lys Arg Ile Ala Leu Asp Gln Lys
130   135   140

Asp Leu Val Ala Val Glu Gly Asp Leu Thr Asn Ile Pro Phe Asp Lys
145   150   155   160

Asn Leu Ile Glu Tyr Leu Lys Lys Ser Ser Glu Val Val Ser Lys Phe
         165   170   175

Glu Ala Gln Lys Gly Gly Ile Glu Asn Asn Thr Arg Leu Thr His Lys
        180   185   190

Asp Leu Ser Ser Glu Gln Lys Glu Ala Lys Val Lys Glu Ala Leu Asp
        195   200   205

Asn Ala Leu Thr Gln Phe Ala Gln Glu Lys Tyr Lys Glu Leu Ile Glu
    210   215   220

Asn Ala His Asp Lys Lys Ser Asp Ala Arg Asn Arg Asp Leu Glu Tyr
225   230   235   240

Val Lys Ser Gly Phe Asn Tyr Leu Ser Gly Tyr Thr Ala Thr Asp His
        245   250   255

Asp Lys Lys Thr Asn Tyr Arg Gly Tyr Tyr Gly Ala Leu Tyr Tyr Lys
        260   265   270

Gly Ser Glu Thr Ala Lys Glu Leu Pro Gln Thr Ser Ala Lys Tyr Lys
        275   280   285

Gly Tyr Trp Asp Phe Met Thr Asp Ala Thr Leu Asp Asn Lys Tyr Thr
        290   295   300

Asp Leu Pro Gly Ile Ala Arg Gln Thr Gln Trp Arg Ser Leu Val Ser
305   310   315   320

Thr Asp Glu Tyr Ala Thr Leu Leu Thr Asp Lys Asn Asn Lys Pro Ser
        325   330   335

Asp Tyr Asn Gly Ala Tyr Gly His Ser Ser Glu Phe Asp Val Asn Phe
        340   345   350

Ala Asp Lys Lys Ile Lys Gly Lys Leu Ile Ser Asn Gln Leu Ser Gly
        355   360   365

Thr Ala Val Thr Ala Lys Glu Arg Tyr Lys Ile Glu Ala Asp Ile His
    370   375   380

Gly Asn Arg Phe Arg Gly Ser Ala Thr Ala Ser Asp Lys Ala Glu Asp
385   390   395   400

Ser Lys Thr Gln His Pro Phe Thr Ser Asp Ala Thr Asn Lys Leu Glu
        405   410   415

Gly Gly Phe Tyr Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu
        420   425   430

Thr Asp Asp Asn Lys Leu Phe Gly Val Phe Gly Ala Lys Arg Asp Lys
435   440   445

Val Glu Lys Thr Glu Ala Ile Leu Asp Ala Tyr Ala Leu Gly Thr Phe
450   455   460

Asn Asn Thr Asn Lys Ala Thr Thr Phe Thr Pro Phe Thr Lys Lys Gln
465   470   475   480

Leu Asp Asn Phe Gly Asn Ala Lys Lys Leu Val Leu Gly Ser Thr Val
                485   490   495

Ile Asn Leu Val Ser Thr Asp Ala Thr Lys Asn Glu Phe Thr Lys Lys
                500   505   510

Phe Thr Lys Asp Lys Pro Thr Ser Ala Thr Asn Lys Ala Gly Glu Thr
                515   520   525

Leu Met Val Asn Asp Glu Val Ile Val Lys Thr Tyr Gly Lys Asn Phe
                530   535   540

Glu Tyr Leu Lys Phe Gly Glu Leu Ser Val Gly Asp Ser His Ser Val
545   550   555   560

Phe Leu Gln Gly Glu Arg Thr Ala Thr Thr Gly Glu Lys Ala Val Pro
                565   570   575

Thr Thr Gly Lys Ala Lys Tyr Leu Gly Asn Trp Val Gly Tyr Ile Thr
                580   585   590

Gly Ala Gly Thr Gly Lys Ser Phe Asn Glu Ala Gln Asp Ile Ala Asp
                595   600   605

Phe Asp Ile Asp Phe Glu Arg Lys Ser Val Lys Gly Lys Leu Thr Thr
                610   615   620

Gln Gly Arg Thr Asp Pro Val Phe Asn Ile Lys Gly Glu Ile Ala Gly
625   630   635   640

Asn Gly Trp Thr Gly Lys Ala Ser Thr Thr Lys Ala Asp Ala Gly Gly
                645   650   655

Tyr Lys Ile Asp Ser Ser Ser Thr Gly Lys Ser Ile Val Ile Glu Asn
                660   665   670

Ala Glu Val Thr Gly Gly Phe Tyr Gly Pro Asn Ala Asn Glu Met Gly
                675   680   685

Gly Ser Phe Thr His Asp Thr Asp Asp Ser Lys Ala Ser Val Val Phe
690   695   700

Gly Thr Lys Arg Gln Gln Glu Val Lys
705   710

<210> 7
<211> 702
<212> PRT

<213> Moraxella catarrhalis

<400> 7
```
Met Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val
 1               5                  10                  15

Leu Leu Thr Ala Cys Gly Gly Ser Gly Gly Ser Asn Pro Pro Ala Pro
            20                  25                  30

Thr Pro Ile Pro Asn Ala Ser Gly Ser Gly Asn Thr Gly Asn Thr Gly
            35                  40                  45

Asn Ala Gly Gly Thr Asp Asn Thr Ala Asn Ala Gly Asn Thr Gly Gly
    50                  55                  60

Thr Asn Ser Gly Thr Gly Ser Ala Asn Thr Pro Glu Pro Lys Tyr Gln
65                  70                  75                  80

Asp Val Pro Thr Glu Lys Asn Glu Lys Asp Lys Val Ser Ser Ile Gln
                85                  90                  95

Glu Pro Ala Met Gly Tyr Gly Met Ala Leu Ser Lys Ile Asn Leu His
            100                 105                 110

Asn Arg Gln Asp Thr Pro Leu Asp Glu Lys Asn Ile Ile Thr Leu Asp
        115                 120                 125

Gly Lys Lys Gln Val Ala Glu Gly Lys Lys Ser Pro Leu Pro Phe Ser
    130                 135                 140

Leu Asp Val Glu Asn Lys Leu Leu Asp Gly Tyr Ile Ala Lys Met Asn
145                 150                 155                 160

Val Ala Asp Lys Asn Ala Ile Gly Asp Arg Ile Lys Lys Gly Asn Lys
                165                 170                 175

Glu Ile Ser Asp Glu Glu Leu Ala Lys Gln Ile Lys Glu Ala Val Arg
            180                 185                 190

Lys Ser His Glu Phe Gln Gln Val Leu Ser Ser Leu Glu Asn Lys Ile
        195                 200                 205

Phe His Ser Asn Asp Gly Thr Thr Lys Ala Thr Thr Arg Asp Leu Lys
    210                 215                 220

Tyr Val Asp Tyr Gly Tyr Tyr Leu Ala Asn Asp Gly Asn Tyr Leu Thr
225                 230                 235                 240

Val Lys Thr Asp Lys Leu Trp Asn Leu Gly Pro Val Gly Gly Val Phe
                245                 250                 255

Tyr Asn Gly Thr Thr Thr Ala Lys Glu Leu Pro Thr Gln Asp Ala Val
            260                 265                 270

Lys Tyr Lys Gly His Trp Asp Phe Met Thr Asp Val Ala Asn Arg Arg
        275                 280                 285

Asn Arg Phe Ser Glu Val Lys Glu Asn Ser Gln Ala Gly Trp Tyr Tyr
    290                 295                 300
```

Gly Ala Ser Ser Lys Asp Glu Tyr Asn Arg Leu Leu Thr Lys Glu Asp
305   310   315   320

Ser Ala Pro Asp Gly His Ser Gly Glu Tyr Gly His Ser Ser Glu Phe
            325   330   335

Thr Val Asn Phe Lys Glu Lys Lys Leu Thr Gly Lys Leu Phe Ser Asn
            340   345   350

Leu Gln Asp Arg His Lys Gly Asn Val Thr Lys Thr Glu Arg Tyr Asp
            355   360   365

Ile Asp Ala Asn Ile His Gly Asn Arg Phe Arg Gly Ser Ala Thr Ala
    370   375   380

Ser Asn Lys Asn Asp Thr Ser Lys His Pro Phe Thr Ser Asp Ala Asn
385   390   395   400

Asn Arg Leu Glu Gly Gly Phe Tyr Gly Pro Lys Gly Glu Glu Leu Ala
            405   410   415

Gly Lys Phe Leu Thr Asn Asp Asn Lys Leu Phe Gly Val Phe Gly Ala
            420   425   430

Lys Arg Glu Ser Lys Ala Glu Glu Lys Thr Glu Ala Ile Leu Asp Ala
            435   440   445

Tyr Ala Leu Gly Thr Phe Asn Thr Ser Asn Ala Thr Thr Phe Thr Pro
    450   455   460

Phe Thr Glu Lys Gln Leu Asp Asn Phe Gly Asn Ala Lys Lys Leu Val
465   470   475   480

Leu Gly Ser Thr Val Ile Asp Leu Val Pro Thr Asp Ala Thr Lys Asn
            485   490   495

Glu Phe Thr Lys Asp Lys Pro Glu Ser Ala Thr Asn Glu Ala Gly Glu
            500   505   510

Thr Leu Met Val Asn Asp Glu Val Ser Val Lys Thr Tyr Gly Lys Asn
            515   520   525

Phe Glu Tyr Leu Lys Phe Gly Glu Leu Ser Ile Gly Gly Ser His Ser
    530   535   540

Val Phe Leu Gln Gly Glu Arg Thr Ala Thr Thr Gly Glu Lys Ala Val
545   550   555   560

Pro Thr Thr Gly Thr Ala Lys Tyr Leu Gly Asn Trp Val Gly Tyr Ile
            565   570   575

Thr Gly Lys Asp Thr Gly Thr Gly Thr Gly Lys Ser Phe Thr Asp Ala
            580   585   590

Gln Asp Val Ala Asp Phe Asp Ile Asp Phe Gly Asn Lys Ser Val Ser
            595   600   605

Gly Lys Leu Ile Thr Lys Gly Arg Gln Asp Pro Val Phe Ser Ile Thr
    610   615   620

Gly Gln Ile Ala Gly Asn Gly Trp Thr Gly Thr Ala Ser Thr Thr Lys
625   630   635   640

Ala Asp Ala Gly Gly Tyr Lys Ile Asp Ser Ser Ser Thr Gly Lys Ser
            645   650   655

Ile Val Ile Lys Asp Ala Asn Val Thr Gly Gly Phe Tyr Gly Pro Asn
            660   665   670

Ala Asn Glu Met Gly Gly Ser Phe Thr His Asn Ala Asp Asp Ser Lys
        675   680   685

Ala Ser Val Val Phe Gly Thr Lys Arg Gln Gln Glu Val Lys
    690   695   700

<210> 8
<211> 714
<212> PRT
<213> Moraxella catarrhalis

<400> 8
Met Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val
1   5   10   15

Leu Leu Thr Ala Cys Gly Gly Ser Gly Gly Ser Asn Pro Pro Ala Pro
            20   25   30

Thr Pro Ile Pro Asn Ala Ser Gly Ser Gly Asn Thr Gly Asn Thr Gly
        35   40   45

Asn Ala Gly Gly Thr Asp Asn Thr Ala Asn Ala Gly Asn Thr Gly Gly
    50   55   60

Thr Ser Ser Gly Thr Gly Ser Ala Ser Thr Ser Glu Pro Lys Tyr Gln
65   70   75   80

Asp Val Pro Thr Thr Pro Asn Asn Lys Glu Gln Val Ser Ser Ile Gln
            85   90   95

Glu Pro Ala Met Gly Tyr Gly Met Ala Leu Ser Lys Ile Asn Leu Tyr
            100   105   110

Asp Gln Gln Asp Thr Pro Leu Asp Ala Lys Asn Ile Ile Thr Leu Asp
        115   120   125

Gly Lys Lys Gln Val Ala Asp Asn Gln Lys Ser Pro Leu Pro Phe Ser
    130   135   140

Leu Asp Val Glu Asn Lys Leu Leu Asp Gly Tyr Ile Ala Lys Met Asn
145   150   155   160

Glu Ala Asp Lys Asn Ala Ile Gly Glu Arg Ile Lys Arg Glu Asn Glu
            165   170   175

Gln Asn Lys Lys Ile Ser Asp Glu Glu Leu Ala Lys Lys Ile Lys Glu
        180   185   190

Asn Val Arg Lys Ser Pro Glu Phe Gln Gln Val Leu Ser Ser Ile Lys
        195   200   205

Ala Lys Thr Phe His Ser Asn Asp Lys Thr Thr Lys Ala Thr Thr Arg
        210   215   220

Asp Leu Lys Tyr Val Asp Tyr Gly Tyr Tyr Leu Val Asn Asp Ala Asn
225   230   235   240

Tyr Leu Thr Val Lys Thr Asp Asn Pro Lys Leu Trp Asn Ser Gly Pro
                245   250   255

Val Gly Gly Val Phe Tyr Asn Gly Ser Thr Thr Ala Lys Glu Leu Pro
                260   265   270

Thr Gln Asp Ala Val Lys Tyr Lys Gly His Trp Asp Phe Met Thr Asp
        275   280   285

Val Ala Lys Lys Arg Asn Arg Phe Ser Glu Val Lys Glu Thr Tyr Gln
        290   295   300

Ala Gly Trp Trp Tyr Gly Ala Ser Ser Lys Asp Glu Tyr Asn Arg Leu
305   310   315   320

Leu Thr Lys Ala Asp Ala Ala Pro Asp Asn Tyr Ser Gly Glu Tyr Gly
                325   330   335

His Ser Ser Glu Phe Thr Val Asn Phe Lys Glu Lys Lys Leu Thr Gly
                340   345   350

Glu Leu Phe Ser Asn Leu Gln Asp Ser His Lys Gln Lys Val Thr Lys
        355   360   365

Thr Lys Arg Tyr Asp Ile Lys Ala Asp Ile His Gly Asn Arg Phe Arg
        370   375   380

Gly Ser Ala Thr Ala Ser Asp Lys Ala Glu Asp Ser Lys Ser Lys His
385   390   395   400

Pro Phe Thr Ser Asp Ala Lys Asp Lys Leu Glu Gly Gly Phe Tyr Gly
                405   410   415

Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Thr Asp Asp Asn Lys
                420   425   430

Leu Phe Gly Val Phe Gly Ala Lys Gln Glu Gly Asn Val Glu Lys Thr
        435   440   445

Glu Ala Ile Leu Asp Ala Tyr Ala Leu Gly Thr Phe Asn Lys Pro Gly
        450   455   460

Thr Thr Asn Pro Ala Phe Thr Ala Asn Ser Lys Lys Glu Leu Asp Asn
465   470   475   480

Phe Gly Asn Ala Lys Lys Leu Val Leu Gly Ser Thr Val Ile Asp Leu
                485   490   495

Val Pro Thr Asp Ala Thr Lys Asp Val Asn Glu Phe Lys Glu Lys Pro
        500   505   510

Lys Ser Ala Thr Asn Lys Ala Gly Glu Thr Leu Met Val Asn Asp Glu
        515   520   525

Val Ser Val Lys Thr Tyr Gly Lys Asn Phe Glu Tyr Leu Lys Phe Gly
        530   535   540

Glu Leu Ser Val Gly Gly Ser His Ser Val Phe Leu Gln Gly Glu Arg
545   550   555   560

Thr Ala Thr Thr Gly Glu Lys Ala Val Pro Thr Thr Gly Lys Ala Lys
            565   570   575

Tyr Leu Gly Asn Trp Val Gly Tyr Ile Thr Gly Ala Asp Ser Ser Lys
        580   585   590

Gly Ser Thr Asp Gly Lys Gly Phe Thr Asp Ala Lys Asp Ile Ala Asp
        595   600   605

Phe Asp Ile Asp Phe Glu Lys Lys Ser Val Asn Gly Lys Leu Thr Thr
    610   615   620

Lys Asp Arg Gln Asp Pro Val Phe Asn Ile Thr Gly Glu Ile Ala Gly
625   630   635   640

Asn Gly Trp Thr Gly Lys Ala Ser Thr Ala Glu Ala Asn Ala Gly Gly
            645   650   655

Tyr Lys Ile Asp Ser Ser Ser Thr Gly Lys Ser Ile Val Ile Lys Asp
        660   665   670

Ala Val Val Thr Gly Gly Phe Tyr Gly Pro Asn Ala Thr Glu Met Gly
        675   680   685

Gly Ser Phe Thr His Asn Ser Gly Asn Lys Gly Lys Val Ser Val Val
    690   695   700

Phe Gly Thr Lys Lys Gln Glu Val Lys Lys
705   710

<210> 9
<211> 708
<212> PRT
<213> Moraxella catarrhalis

<400> 9
Met Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val
  1   5   10   15

Leu Leu Thr Ala Cys Gly Gly Ser Ser Gly Gly Phe Asn Pro Pro Ala
            20   25   30

Ser Thr Pro Ile Pro Asn Ala Gly Asn Ser Gly Asn Ala Gly Asn Ala
        35   40   45

Gly Asn Ala Gly Gly Thr Gly Gly Ala Asn Ser Gly Ala Gly Asn Ala
    50   55   60

Gly Gly Thr Gly Gly Ala Asn Ser Gly Ala Gly Ser Ala Ser Thr Pro
  65   70   75   80

Glu Pro Lys Tyr Lys Asp Val Pro Thr Asp Glu Asn Lys Lys Ala Glu
            85   90   95

Val Ser Gly Ile Gln Glu Pro Ala Met Gly Tyr Gly Val Glu Leu Lys
          100   105   110

Leu Arg Asn Trp Ile Pro Gln Ala Gln Glu Glu His Ala Lys Ile Asn
        115   120   125

Thr Asn Asp Val Val Lys Leu Asp Asn Asp Leu Lys His Asn Pro Phe
        130   135   140

Asp Asn Ser Ile Trp Gln Asn Ile Lys Asn Ser Lys Glu Val Gln Thr
145   150   155   160

Val Tyr Asn Gln Glu Lys Gln Asn Ile Glu Asp Gln Ile Lys Arg Glu
          165   170   175

Asn Lys Gln Arg Pro Asp Lys Lys Asp Asp Val Ala Leu Gln Ala Tyr
        180   185   190

Ile Glu Lys Val Leu Asp Asp Arg Leu Thr Glu Leu Ala Lys Pro Ile
        195   200   205

Tyr Lys Lys Asn Thr Asn Tyr Ser His Asp Lys Gln Asn Lys Ala Arg
    210   215   220

Thr Arg Asp Leu Lys Tyr Val Arg Ser Gly Tyr Ile Tyr Arg Ser Gly
225   230   235   240

Tyr Ser Asn Ile Ile Pro Lys His Ile Ala Lys Thr Gly Phe Asp Gly
        245   250   255

Ala Leu Phe Tyr Gln Gly Ser Gln Thr Ala Lys Gln Leu Pro Val Ser
        260   265   270

Gln Val Lys Tyr Lys Gly Thr Trp Asp Phe Met Thr Asp Ala Lys Lys
        275   280   285

Gly Gln Ser Phe Ser Ser Phe Gly Thr Ser Gln Arg Leu Ala Gly Asp
        290   295   300

Arg Tyr Ser Ala Met Ser Tyr His Glu Tyr Pro Ser Leu Leu Thr Asp
305   310   315   320

Glu Lys Asn Lys Pro Asp Asn Tyr Asn Gly Glu Tyr Gly His Ser Ser
            325   330   335

Glu Phe Thr Val Asp Phe Ser Lys Lys Ser Leu Lys Gly Glu Leu Ser
        340   345   350

Ser Asn Leu Gln Asp Gly His Lys Gly Ser Val Asn Lys Thr Lys Arg
        355   360   365

```
Tyr Asp Ile Asp Ala Asn Ile Tyr Gly Asn Arg Phe Arg Gly Ser Ala
    370             375             380
Thr Ala Ser Asp Thr Thr Glu Ala Ser Lys Ser Lys His Pro Phe Thr
385             390             395             400
Ser Asp Ala Lys Asn Ser Leu Glu Gly Gly Phe Tyr Gly Pro Asn Ala
            405             410             415
Glu Glu Leu Ala Gly Lys Phe Leu Thr Asn Asp Asn Lys Leu Phe Gly
            420             425             430
Val Phe Gly Ala Lys Arg Glu Ser Glu Ala Lys Glu Lys Thr Glu Ala
        435             440             445
Ile Leu Asp Ala Tyr Ala Leu Gly Thr Phe Asn Lys Pro Gly Thr Thr
    450             455             460
Asn Pro Ala Phe Thr Ala Asn Ser Lys Lys Glu Leu Asp Asn Phe Gly
465             470             475             480
Asn Ala Lys Lys Leu Val Leu Gly Ser Thr Val Ile Asp Leu Val Pro
            485             490             495
Thr Gly Ala Thr Lys Asp Val Asn Glu Phe Lys Glu Lys Pro Lys Ser
        500             505             510
Ala Thr Asn Lys Ala Gly Glu Thr Leu Met Val Asn Asp Glu Val Ile
        515             520             525
Val Lys Thr Tyr Gly Tyr Gly Arg Asn Phe Glu Tyr Leu Lys Phe Gly
    530             535             540
Glu Leu Ser Ile Gly Gly Ser His Ser Val Phe Leu Gln Gly Glu Arg
545             550             555             560
Thr Ala Glu Lys Ala Val Pro Thr Glu Gly Thr Ala Lys Tyr Leu Gly
            565             570             575
Asn Trp Val Gly Tyr Ile Thr Gly Lys Asp Thr Gly Thr Ser Thr Gly
            580             585             590
Lys Ser Phe Asn Glu Ala Gln Asp Ile Ala Asp Phe Asp Ile Asp Phe
        595             600             605
Glu Arg Lys Ser Val Lys Gly Lys Leu Thr Thr Gln Gly Arg Gln Asp
    610             615             620
Pro Val Phe Asn Ile Thr Gly Gln Ile Ala Gly Asn Gly Trp Thr Gly
625             630             635             640
Thr Ala Ser Thr Ala Lys Ala Asn Val Gly Gly Tyr Lys Ile Asp Ser
            645             650             655
Ser Ser Thr Gly Lys Ser Ile Val Ile Glu Asn Ala Lys Val Thr Gly
            660             665             670
```

Gly Phe Tyr Gly Pro Asn Ala Asn Glu Met Gly Gly Ser Phe Thr His
        675   680   685

Asp Thr Asp Asp Ser Lys Ala Ser Val Val Phe Gly Thr Lys Arg Gln
    690   695   700

Glu Glu Val Lys
705

<210> 10
<211> 8266
<212> DNA
<213> Moraxella catarrhalis

<400> 10
gatgcctgcc ttgtgattgg ttggggtgta tcggtgtatc aaagtgcaaa agccaacagg 60
tggtcattga tgaatcaatc aaaacaaaac aacaaatcca aaaaatccaa acaagtatta 120
aaacttagtg ccttgtcttt gggtctgctt aacatcacgc aggtggcact ggcaaacaca 180
acggccgata aggcggaggc aacagataag acaaaccttg ttgttgtctt ggatgaaact 240
gttgtaacag cgaagaaaaa cgcccgtaaa gccaacgaag ttacagggct tggtaaggtg 300
gtcaaaactg ccgagaccat caataaagaa caagtgctaa acattcgaga cttaacacgc 360
tatgaccctg gcattgctgt ggttgagcaa ggtcgtgggg caagctcagg ctattctatt 420
cgtggtatgg ataaaaatcg tgtggcggta ttggttgatg catcaatca agcccagcac 480
tatgccctac aaggccctgt ggcaggcaaa aattatgccg caggtggggc aatcaacgaa 540
atagaatacg aaaatgtccg ctccgttgag attagtaaag gtgcaaattc aagtgaatac 600
ggctctgggg cattatctgg ctctgtggca tttgttacca aaaccgccga tgacatcatc 660
aaagatggta agattggggg cgtgcagacc aaaaccgcct atgccagtaa aaataacgca 720
tgggttaatt ctgtggcagc agcaggcaag gcaggttctt ttagcggtct tatcatctac 780
accgaccgcc gtggtcaaga atacaaggca catgatgatg cctatcaggg tagccaaagt 840
tttgatagag cggtggcaac cactgaccca aàtaaccgaa cattttttaat agcaaatgaa 900
tgtgccaatg gtaattatga ggcgtgtgct gctggcggtc aaaccaaact tcaagccaag 960
ccaaccaatg tgcgtgataa ggtcaatgtc aaagattata caggtcctaa ccgccttatc 1020
ccaaacccac tcacccaaga cagcaaatcc ttactgcttc gcccaggtta tcagctaaac 1080
gataagcact atgtcggtgg tgtgtatgaa atcaccaaac aaaactacgc catgcaagat 1140
aaaaccgtgc ctgcttatct ggcggttcat gacattgaaa aatcaaggct cagcaaccat 1200
gcccaagcca atggctatta tcaaggcaat aatcttggtg aacgcattcg tgataccatt 1260
gggccagatt caggttatgg catcaactat gctcatggcg tattttatga tgaaaaacac 1320
caaaaagacc gcctagggct tgaatatgtt tatgacagca aaggtgaaaa taaatggttt 1380
gatgatgtgc gtgtgtctta tgataagcaa gacattacgc tacgcagcca gctgaccaac 1440
acgcactgtt caacctatcc gcacattgac aaaaattgta cgcctgatgt caataaacct 1500
ttttcggtaa aagaggtgga taacaatgcc tacaaagaac agcacaattt aatcaaagcc 1560
gtctttaaca aaaaaatggc gttgggcagt acgcatcatc acatcaacct gcaagttggc 1620
tatgataaat tcaattcaag cctgagccgt gtagaatatc gtttggcaac ccatcagtct 1680
tatcaaaaac ttgattacac cccaccaagt aacccttttgc cagataagtt taagcccatt 1740
ttaggttcaa acaacaaacc catttgcctt gatgcttatg ttatggtca tgaccatcca 1800
caggcttgta cgccaaaaaa cagcacttat caaaattttg ccatcaaaaa aggcatagag 1860
caatacaacc aaaaaaccaa taccgataag attgattatc aagccatcat tgaccaatat 1920
gataaacaaa accccaacag caccctaaaa ccctttgaga aaatcaaaca aagtttgggg 1980
caagaaaaat acaacaagat agacgaactt ggctttaaag cttataaaga tttacgcaac 2040
gaatgggcgg ttggactaa tgacaacagc caacaaaatg ccaataaagg cacggataat 2100
atctatcagc caaatcaagc aactgtggtc aaagatgaca atgtaaata tagcgagacc 2160
aacagctatg ctgattgctc aaccactcgc cacatcagtg gtgataatta tttcatcgct 2220
ttaaaagaca acatgaccat caataaatat gttgatttgg ggctgggtgc tcgctatgac 2280
agaatcaaac acaaatctga tgtgcctttg gtagacaaca gtgccagcaa ccagctgtct 2340
tggaattttg gcgtggtcgt caagcccacc aattggctgg acatcgctta tagaagctcg 2400
caaggctttc gcatgccaag ttttttctgaa atgtatggcg aacgctttgg cgtaaccatc 2460
ggtaaaggca cgcaacatgg ctgtaagggt ctttattaca tttgtcagca gactgtccat 2520

```
caaaccaagc taaaacctga aaaatccttt aaccaagaaa tcggagcgac tttacataac 2580
cacttaggca gtcttgaggt tagttatttt aaaaatcgct ataccgattt gattgttggt 2640
aaaagtgaag agattagaac cctaacccaa ggtgataatg caggcaaaca gcgtggtaaa 2700
ggtgatttgg gctttcataa tggacaagat gctgatttga caggaattaa cattcttggc 2760
agacttgacc taaacgctgc caatagtcgc cttccctatg gattatactc aacactggct 2820
tataacaaag ttgatgttaa aggaaaaacc ttaaacccaa cttttggcagg aacaaacata 2880
ctgtttgatg ccatccagcc atctcgttat gtggtggggc ttggctatga tgccccaagc 2940
caaaaatggg gagcaaacgc catatttacc cattctgatg ccaaaaatcc aagcgagctt 3000
ttggcagata agaacttagg taatggcaac attcaaacaa aacaagccac caaagcaaaa 3060
tccacgccgt ggcaaacact tgatttgtca ggttatgtaa acataaaaga taattttacc 3120
ttgcgtgctg gcgtgtacaa tgtatttaat acctattaca ccacttggga ggctttacgc 3180
caaacagcaa aagggggcggt caatcagcat acaggactga gccaagataa gcattatggt 3240
cgctatgccg ctcctggacg caattaccaa ttggcacttg aaatgaagtt ttaaccagtg 3300
gctttgatgt gattttggca tgccaaatcc caatcaacca atgaataaag ccccattac 3360
catgagggct ttattttatc atcgctgagt atgctcttag cggtcatcac tcagattagt 3420
cattaattta ttagcgatta atttattagt aatcacgctg ctctttgatg attttaagtg 3480
atgggtattc aagaacgatg tcatactcag caccgttttt ataggcttct acttcaaaga 3540
caggcttgcc taaaaagtca tcaacttcta tatcgccgac ttgatagcca cgagcagcaa 3600
gcatttgaat ggcttttttga cgattttggg caaagttgct gtcgccataa gcttgtgctt 3660
taatacggtc gttagcaact gcggtggtag agataccaac ggcaggcaac aaaacagcag 3720
cacttagtac gccagccaac agtttattgg ttaaattttt catagtagtt tcctaattat 3780
tatcattgta attcatgttt atcgttataa acaatcgtta taaataactg tgtcgtgata 3840
accattaatc acaagtgggt taaatgcctt ttgcccaatg gcaaataggc acaatgctct 3900
gcttgttcta tgatggtcta ttatgatcat cattttattg acctattttt ttaatcgtaa 3960
tgtttgtttg atgttagtat aaatttttatc aatcaaacaa tcacaaatta tatcaatcat 4020
agacggtaaa caggcttcat attttacgca tatttcccca gatgtctgta gtgtttcata 4080
gatgatttgt aaaacaattg tcggtcatta ttatcaattg taaactgatg gctaatttgt 4140
aaccttatgg ctaatgataa tatgaataaa gcgttatact gtatcaaaga atgagtaaaa 4200
accatcaatg gtatcttatt tatcatcagg ttgtgttaat aagatgccaa ttaagcgact 4260
aatttttgtaa attaattaat aatcattcat atttgtattt ttaaataccaa taaaaaatgg 4320
taaaatatgc tcgcttttt gataggagct gtcatgacaa tcacgcctgt ttataccaca 4380
ttcacccccca ccaaaacacc cataaaattt tttatggctg cttgacttt tctaatcgct 4440
catatcagcc atgccgatga tggtcgcacc gacaatcaag agctaatcaa tcaagaaata 4500
gccacccttg aacccatcat taaccatgct cagcctgagt tattgtccca tgatgcatta 4560
acaccaaaaa tagaaccaat actggcacaa acaccaaatc ctgccgaaga tacgctcatc 4620
gccgatgagg cgttactgct tgataaccct gatttgctca atcacgccct aaattctgct 4680
gtcatgacca atcatatggc aggcgttcac gcattattgc ccattatca aaaactgccc. 4740
aaagaccatc aaaatggcat tttacttggg tatgccaatg ccttggctgc tttggataag 4800
ggcaacgcca aaaaagccat tgatgagcta cgtcgcatca tcgccatcat gcctgaatat 4860
aatgtggtgc gttttcatct ggcaagggca ttatttatgg acaaacaaaa tgaagccgcc 4920
cttgaccagt ttaataaaatt acatgctgac aacttgccag aggaggtgcg gcaggttgtt 4980
gggcagtaca gacaagcgct aaaacaacga gattcatgga catggcaagt aggcatgaat 5040
ctggccaaag aagacaacat caatcaaacc cccaaaaaca ccacgcaagg tcaatggact 5100
tttgacaaac ccattgacgc catcacccta agctaccaat tggggcgga taaaaagtgg 5160
tctttgccca aagggcata tgtgggagcg aacgcccaaa tctatggcaa acatcatcaa 5220
aatcacaaaa aatacaacga ccattggggc agactggggg caaatttggg ctttgctgat 5280
gccaaaaaag accttagcat tgagacctat ggtgaaaaaa gatttttatgg gcatgagcgt 5340
tataccgaca ccattggcat acgcatgtcg gttgattata gaatcaaccc aaaatttcaa 5400
agcctaaacg ccatagacat atcacgccta accaaccatc ggacgcctag ggctgacagt 5460
aataacactt tatacagtac ctcattgatt tattacccaa atgccacacg ctattatctt 5520
ttgggggcag acttttatga tgaaaaagtg ccacaagacc catctgacag ttatcaacgc 5580
cgtggcatac gcacagcgtg ggggcaagaa tgggcgggtg gtctttcaag ccgtgcccaa 5640
atcagcatca acaaacgcca ttaccaaggg gcaaacctaa ccagcggtgg acaaattcgc 5700
catgataaac agatgcaagc gtctttatcg ctttggcaca gagacattca caaatggggc 5760
atcacgccac ggctgaccat cagcacaaac atcaataaaa gcaatgacat caaggcaaat 5820
tatcacaaaa atcaaatgtt tgttgagttt agtcgcattt tttgatggga taagcacgcc 5880
ctactttttgt ttttgtaaaa aaatgtgcca tcatagacaa tatcaagaaa aaatcaagaa 5940
aaaaagatta caaatttaat gataattgtt attgtttatg ttattatttta tcaatgtaaa 6000
tttgccgtat tttgtctatc ataaatgcat ttatcaaatg ctcaaataaa tacgccaaat 6060
```

```
gcacattgtc agcatgccaa aataggcatc aacagacttt tttagataat accatcaacc 6120
catcagagga ttattttatg aaacacattc ctttaaccac actgtgtgtg gcaatctctg 6180
ccgtcttatt aaccgcttgt ggtggcagtg gtggttcaaa tccacctgct cctacgccca 6240
ttccaaatgc tagcggttca ggtaatactg gcaacactgg taatgctggc ggtactgata 6300
atacagccaa tgcaggtaat acaggcggta caaactctgg tacaggcagt gccaacacac 6360
cagagccaaa atatcaagat gtaccaactg agaaaaatga aaaagataaa gtttcatcca 6420
ttcaagaacc tgccatgggt tatggcatgg ctttgagtaa aattaatcta cacaaccgac 6480
aagacacgcc attagatgaa aaaaatatca ttaccttaga cggtaaaaaa caagttgcag 6540
aaggtaaaaa atcgccattg ccattttcgt tagatgtaga aaataaattg cttgatggct 6600
atatagcaaa aatgaatgta gcggataaaa atgccattgg tgacagaatt aagaaaggta 6660
ataaagaaat ctccgatgaa gaacttgcca aacaaatcaa agaagctgtg cgtaaaagcc 6720
atgagtttca gcaagtatta tcatcactgg aaaacaaaat ttttcattca aatgacggaa 6780
caaccaaagc aaccacacga gatttaaaat atgttgatta tggttactac ttggcgaatg 6840
atggcaatta tctaaccgtc aaaacagaca aactttggaa tttaggccct gtgggtggtg 6900
tgttttataa tggcacaacg accgccaaag agttgcccac acaagatgcg gtcaaatata 6960
aaggacattg ggactttatg accgatgttg ccaacagaag aaaccgattt agcgaagtga 7020
aagaaaactc tcaagcaggc tggtattatg gagcatcttc aaaagatgaa tacaaccgct 7080
tattaactaa agaagactct gcccctgatg gtcatagcgg tgaatatggc catagcagtg 7140
agtttactgt taattttaag gaaaaaaat aacaggtaa gctgtttagt aacctacaag 7200
accgccataa gggcaatgtt acaaaaaccg aacgctatga catcgatgcc aatatccacg 7260
gcaaccgctt ccgtggcagt gccaccgcaa gcaataaaaa tgacacaagc aaacacccct 7320
ttaccagtga tgccaacaat aggctagaag gtggtttta tgggccaaaa ggcgaggagc 7380
tggcaggtaa attcttaacc aatgacaaca aactctttgg cgtctttggt gctaaacgag 7440
agagtaaagc tgaggaaaaa accgaagcca tcttagatgc ctatgcactt gggacattta 7500
atacaagtaa cgcaaccaca ttcaccccat ttaccgaaaa acaactggat aactttggca 7560
atgccaaaaa attggtctta ggttctaccg tcattgattt ggtgcctact gatgccacca 7620
aaaatgaatt caccaaagac aagccagagt ctgccacaaa cgaagcgggc gagactttga 7680
tggtgaatga tgaagttagc gtcaaaacct atggcaaaaa ctttgaatac ctaaaatttg 7740
gtgagcttag tatcggtggt agccatagcg tctttttaca aggcgaacgc accgctacca 7800
caggcgagaa agccgtacca accacaggca cagccaaata tttgggggaac tgggtaggat 7860
acatcacagg aaaggacaca ggaacgggca caggaaaaag ctttaccgat gcccaagatg 7920
ttgctgattt tgacattgat tttggaaata aatcagtcag cggtaaactt atcaccaaag 7980
gccgccaaga ccctgtattt agcatcacag gtcaaatcgc aggcaatggc tggacaggga 8040
cagccagcac caccaaagcg gacgcaggag ctacaagat agattctagc agtacaggca 8100
aatccatcgc catcaaagat gccaatgtta caggggggcctt ttatggtcca aatgcaaacg 8160
agatgggcgg gtcatttaca cacaacgccg atgacagcaa agcctctgtg gtctttggca 8220
caaaaagaca acaagaagtt aagtagtaat ttaaacacaa tgtttg        8266
```

<210> 11
<211> 2288
<212> PRT
<213> Moraxella catarrhalis

<400> 11
Met Asn Gln Ser Lys Gln Asn Asn Lys Ser Lys Lys Ser Lys Gln Val
1   5   10   15

Leu Lys Leu Ser Ala Leu Ser Leu Gly Leu Leu Asn Ile Thr Gln Val
            20   25   30

Ala Leu Ala Asn Thr Thr Ala Asp Lys Ala Glu Ala Thr Asp Lys Thr
        35   40   45

Asn Leu Val Val Val Leu Asp Glu Thr Val Val Thr Ala Lys Lys Asn
    50   55   60

Ala Arg Lys Ala Asn Glu Val Thr Gly Leu Gly Lys Val Val Lys Thr
65   70   75   80

Ala Glu Thr Ile Asn Lys Glu Gln Val Leu Asn Ile Arg Asp Leu Thr
                85   90   95

Arg Tyr Asp Pro Gly Ile Ala Val Val Glu Gln Gly Arg Gly Ala Ser
            100   105   110

Ser Gly Tyr Ser Ile Arg Gly Met Asp Lys Asn Arg Val Ala Val Leu
        115   120   125

Val Asp Gly Ile Asn Gln Ala Gln His Tyr Ala Leu Gln Gly Pro Val
    130   135   140

Ala Gly Lys Asn Tyr Ala Ala Gly Gly Ala Ile Asn Glu Ile Glu Tyr
145   150   155   160

Glu Asn Val Arg Ser Val Glu Ile Ser Lys Gly Ala Asn Ser Ser Glu
            165   170   175

Tyr Gly Ser Gly Ala Leu Ser Gly Ser Val Ala Phe Val Thr Lys Thr
        180   185   190

Ala Asp Asp Ile Ile Lys Asp Gly Lys Asp Trp Gly Val Gln Thr Lys
        195   200   205

Thr Ala Tyr Ala Ser Lys Asn Asn Ala Trp Val Asn Ser Val Ala Ala
    210   215   220

Ala Gly Lys Ala Gly Ser Phe Ser Gly Leu Ile Ile Tyr Thr Asp Arg
225   230   235   240

Arg Gly Gln Glu Tyr Lys Ala His Asp Asp Ala Tyr Gln Gly Ser Gln
            245   250   255

Ser Phe Asp Arg Ala Val Ala Thr Thr Asp Pro Asn Asn Arg Thr Phe
            260   265   270

Leu Ile Ala Asn Glu Cys Ala Asn Gly Asn Tyr Glu Ala Cys Ala Ala
    275   280   285

Gly Gly Gln Thr Lys Leu Gln Ala Lys Pro Thr Asn Val Arg Asp Lys
    290   295   300

Val Asn Val Lys Asp Tyr Thr Gly Pro Asn Arg Leu Ile Pro Asn Pro
305   310   315   320

Leu Thr Gln Asp Ser Lys Ser Leu Leu Leu Arg Pro Gly Tyr Gln Leu
            325   330   335

Asn Asp Lys His Tyr Val Gly Gly Val Tyr Glu Ile Thr Lys Gln Asn
            340   345   350

Tyr Ala Met Gln Asp Lys Thr Val Pro Ala Tyr Leu Ala Val His Asp
        355   360   365

Ile Glu Lys Ser Arg Leu Ser Asn His Ala Gln Ala Asn Gly Tyr Tyr
    370   375   380

Gln Gly Asn Asn Leu Gly Glu Arg Ile Arg Asp Thr Ile Gly Pro Asp
385   390   395   400

Ser Gly Tyr Gly Ile Asn Tyr Ala His Gly Val Phe Tyr Asp Glu Lys
            405   410   415

His Gln Lys Asp Arg Leu Gly Leu Glu Tyr Val Tyr Asp Ser Lys Gly
        420   425   430

Glu Asn Lys Trp Phe Asp Asp Val Arg Val Ser Tyr Asp Lys Gln Asp
        435   440   445

Ile Thr Leu Arg Ser Gln Leu Thr Asn Thr His Cys Ser Thr Tyr Pro
    450   455   460

His Ile Asp Lys Asn Cys Thr Pro Asp Val Asn Lys Pro Phe Ser Val
465   470   475   480

Lys Glu Val Asp Asn Asn Ala Tyr Lys Glu Gln His Asn Leu Ile Lys
            485   490   495

Ala Val Phe Asn Lys Lys Met Ala Leu Gly Ser Thr His His His Ile
            500   505   510

Asn Leu Gln Val Gly Tyr Asp Lys Phe Asn Ser Ser Leu Ser Arg Val
        515   520   525

Glu Tyr Arg Leu Ala Thr His Gln Ser Tyr Gln Lys Leu Asp Tyr Thr
    530   535   540

Pro Pro Ser Asn Pro Leu Pro Asp Lys Phe Lys Pro Ile Leu Gly Ser
545   550   555   560

Asn Asn Lys Pro Ile Cys Leu Asp Ala Tyr Gly Tyr Gly His Asp His
            565   570   575

Pro Gln Ala Cys Asn Ala Lys Asn Ser Thr Tyr Gln Asn Phe Ala Ile
            580   585   590

Lys Lys Gly Ile Glu Gln Tyr Asn Gln Lys Thr Asn Thr Asp Lys Ile
        595   600   605

Asp Tyr Gln Ala Ile Ile Asp Gln Tyr Asp Lys Gln Asn Pro Asn Ser
    610   615   620

Thr Leu Lys Pro Phe Glu Lys Ile Lys Gln Ser Leu Gly Gln Glu Lys
625   630   635   640

Tyr Asn Lys Ile Asp Glu Leu Gly Phe Lys Ala Tyr Lys Asp Leu Arg
            645   650   655

Asn Glu Trp Ala Gly Trp Thr Asn Asp Asn Ser Gln Gln Asn Ala Asn
            660   665   670

Lys Gly Thr Asp Asn Ile Tyr Gln Pro Asn Gln Ala Thr Val Val Lys
    675   680   685

Asp Asp Lys Cys Lys Tyr Ser Glu Thr Asn Ser Tyr Ala Asp Cys Ser
  690   695   700

Thr Thr Arg His Ile Ser Gly Asp Asn Tyr Phe Ile Ala Leu Lys Asp
705   710   715   720

Asn Met Thr Ile Asn Lys Tyr Val Asp Leu Gly Leu Gly Ala Arg Tyr
        725   730   735

Asp Arg Ile Lys His Lys Ser Asp Val Pro Leu Val Asp Asn Ser Ala
      740   745   750

Ser Asn Gln Leu Ser Trp Asn Phe Gly Val Val Val Lys Pro Thr Asn
      755   760   765

Trp Leu Asp Ile Ala Tyr Arg Ser Ser Gln Gly Phe Arg Met Pro Ser
  770   775   780

Phe Ser Glu Met Tyr Gly Glu Arg Phe Gly Val Thr Ile Gly Lys Gly
785   790   795   800

Thr Gln His Gly Cys Lys Gly Leu Tyr Tyr Ile Cys Gln Gln Thr Val
        805   810   815

His Gln Thr Lys Leu Lys Pro Glu Lys Ser Phe Asn Gln Glu Ile Gly
      820   825   830

Ala Thr Leu His Asn His Leu Gly Ser Leu Glu Val Ser Tyr Phe Lys
      835   840   845

Asn Arg Tyr Thr Asp Leu Ile Val Gly Lys Ser Glu Glu Ile Arg Thr
  850   855   860

Leu Thr Gln Gly Asp Asn Ala Gly Lys Gln Arg Gly Lys Gly Asp Leu
865   870   875   880

Gly Phe His Asn Gly Gln Asp Ala Asp Leu Thr Gly Ile Asn Ile Leu
        885   890   895

Gly Arg Leu Asp Leu Asn Ala Ala Asn Ser Arg Leu Pro Tyr Gly Leu
      900   905   910

Tyr Ser Thr Leu Ala Tyr Asn Lys Val Asp Val Lys Gly Lys Thr Leu
      915   920   925

Asn Pro Thr Leu Ala Gly Thr Asn Ile Leu Phe Asp Ala Ile Gln Pro
  930   935   940

Ser Arg Tyr Val Val Gly Leu Gly Tyr Asp Ala Pro Ser Gln Lys Trp
945   950   955   960

Gly Ala Asn Ala Ile Phe Thr His Ser Asp Ala Lys Asn Pro Ser Glu
        965   970   975

Leu Leu Ala Asp Lys Asn Leu Gly Asn Gly Asn Ile Gln Thr Lys Gln
      980   985   990

Ala Thr Lys Ala Lys Ser Thr Pro Trp Gln Thr Leu Asp Leu Ser Gly
      995   1000   1005

Tyr Val Asn Ile Lys Asp Asn Phe Thr Leu Arg Ala Gly Val Tyr Asn
   1010   1015   1020

Val Phe Asn Thr Tyr Tyr Thr Thr Trp Glu Ala Leu Arg Gln Thr Ala
1025   1030   1035   1040

Lys Gly Ala Val Asn Gln His Thr Gly Leu Ser Gln Asp Lys His Tyr
       1045   1050   1055

Gly Arg Tyr Ala Ala Pro Gly Arg Asn Tyr Gln Leu Ala Leu Glu Met
     1060   1065   1070

Lys Phe Met Leu Ala Phe Leu Ile Gly Ala Val Met Thr Ile Thr Pro
    1075   1080   1085

Val Tyr Thr Thr Phe Thr Pro Thr Lys Thr Pro Ile Lys Phe Phe Met
   1090   1095   1100

Ala Gly Leu Thr Phe Leu Ile Ala His Ile Ser His Ala Asp Asp Gly
1105   1110   1115   1120

Arg Thr Asp Asn Gln Glu Leu Ile Asn Gln Glu Ile Ala Thr Leu Glu
       1125   1130   1135

Pro Ile Ile Asn His Ala Gln Pro Glu Leu Leu Ser His Asp Ala Leu
       1140   1145   1150

Thr Pro Lys Ile Glu Pro Ile Leu Ala Gln Thr Pro Asn Pro Ala Glu
       1155   1160   1165

Asp Thr Leu Ile Ala Asp Glu Ala Leu Leu Leu Asp Asn Pro Asp Leu
   1170   1175   1180

Leu Asn His Ala Leu Asn Ser Ala Val Met Thr Asn His Met Ala Gly
1185   1190   1195   1200

Val His Ala Leu Leu Pro Ile Tyr Gln Lys Leu Pro Lys Asp His Gln
       1205   1210   1215

Asn Gly Ile Leu Leu Gly Tyr Ala Asn Ala Leu Ala Ala Leu Asp Lys
       1220   1225   1230

Gly Asn Ala Lys Lys Ala Ile Asp Glu Leu Arg Arg Ile Ile Ala Ile
     1235   1240   1245

Met Pro Glu Tyr Asn Val Val Arg Phe His Leu Ala Arg Ala Leu Phe
   1250   1255   1260

Met Asp Lys Gln Asn Glu Ala Ala Leu Asp Gln Phe Asn Lys Leu His
1265   1270   1275   1280

Ala Asp Asn Leu Pro Glu Glu Val Arg Gln Val Val Gly Gln Tyr Arg
        1285   1290   1295

Gln Ala Leu Lys Gln Arg Asp Ser Trp Thr Trp Gln Val Gly Met Asn
            1300   1305   1310

Leu Ala Lys Glu Asp Asn Ile Asn Gln Thr Pro Lys Asn Thr Thr Gln
        1315   1320   1325

Gly Gln Trp Thr Phe Asp Lys Pro Ile Asp Ala Ile Thr Leu Ser Tyr
    1330   1335   1340

Gln Leu Gly Ala Asp Lys Lys Trp Ser Leu Pro Lys Gly Ala Tyr Val
1345   1350   1355   1360

Gly Ala Asn Ala Gln Ile Tyr Gly Lys His His Gln Asn His Lys Lys
            1365   1370   1375

Tyr Asn Asp His Trp Gly Arg Leu Gly Ala Asn Leu Gly Phe Ala Asp
            1380   1385   1390

Ala Lys Lys Asp Leu Ser Ile Glu Thr Tyr Gly Glu Lys Arg Phe Tyr
        1395   1400   1405

Gly His Glu Arg Tyr Thr Asp Thr Ile Gly Ile Arg Met Ser Val Asp
    1410   1415   1420

Tyr Arg Ile Asn Pro Lys Phe Gln Ser Leu Asn Ala Ile Asp Ile Ser
1425   1430   1435   1440

Arg Leu Thr Asn His Arg Thr Pro Arg Ala Asp Ser Asn Asn Thr Leu
            1445   1450   1455

Tyr Ser Thr Ser Leu Ile Tyr Tyr Pro Asn Ala Thr Arg Tyr Tyr Leu
            1460   1465   1470

Leu Gly Ala Asp Phe Tyr Asp Glu Lys Val Pro Gln Asp Pro Ser Asp
        1475   1480   1485

Ser Tyr Gln Arg Arg Gly Ile Arg Thr Ala Trp Gly Gln Glu Trp Ala
    1490   1495   1500

Gly Gly Leu Ser Ser Arg Ala Gln Ile Ser Ile Asn Lys Arg His Tyr
1505   1510   1515   1520

Gln Gly Ala Asn Leu Thr Ser Gly Gly Gln Ile Arg His Asp Lys Gln
            1525   1530   1535

Met Gln Ala Ser Leu Ser Leu Trp His Arg Asp Ile His Lys Trp Gly
            1540   1545   1550

Ile Thr Pro Arg Leu Thr Ile Ser Thr Asn Ile Asn Lys Ser Asn Asp
        1555   1560   1565

Ile Lys Ala Asn Tyr His Lys Asn Gln Met Phe Val Glu Phe Ser Arg
    1570   1575   1580

Ile Phe Met Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser
1585   1590   1595   1600

Ala Val Leu Leu Thr Ala Cys Gly Gly Ser Gly Gly Ser Asn Pro Pro
       1605   1610   1615

Ala Pro Thr Pro Ile Pro Asn Ala Ser Gly Ser Gly Asn Thr Gly Asn
      1620   1625   1630

Thr Gly Asn Ala Gly Gly Thr Asp Asn Thr Ala Asn Ala Gly Asn Thr
    1635   1640   1645

Gly Gly Thr Asn Ser Gly Thr Gly Ser Ala Asn Thr Pro Glu Pro Lys
    1650   1655   1660

Tyr Gln Asp Val Pro Thr Glu Lys Asn Glu Lys Asp Lys Val Ser Ser
1665   1670   1675   1680

Ile Gln Glu Pro Ala Met Gly Tyr Gly Met Ala Leu Ser Lys Ile Asn
        1685   1690   1695

Leu His Asn Arg Gln Asp Thr Pro Leu Asp Glu Lys Asn Ile Ile Thr
    1700   1705   1710

Leu Asp Gly Lys Lys Gln Val Ala Glu Gly Lys Lys Ser Pro Leu Pro
    1715   1720   1725

Phe Ser Leu Asp Val Glu Asn Lys Leu Leu Asp Gly Tyr Ile Ala Lys
     1730   1735   1740

Met Asn Val Ala Asp Lys Asn Ala Ile Gly Asp Arg Ile Lys Lys Gly
1745   1750   1755   1760

Asn Lys Glu Ile Ser Asp Glu Glu Leu Ala Lys Gln Ile Lys Glu Ala
      1765   1770   1775

Val Arg Lys Ser His Glu Phe Gln Gln Val Leu Ser Ser Leu Glu Asn
     1780   1785   1790

Lys Ile Phe His Ser Asn Asp Gly Thr Thr Lys Ala Thr Thr Arg Asp
    1795   1800   1805

Leu Lys Tyr Val Asp Tyr Gly Tyr Tyr Leu Ala Asn Asp Gly Asn Tyr
    1810   1815   1820

Leu Thr Val Lys Thr Asp Lys Leu Trp Asn Leu Gly Pro Val Gly Gly
1825   1830   1835   1840

Val Phe Tyr Asn Gly Thr Thr Thr Ala Lys Glu Leu Pro Thr Gln Asp
     1845   1850   1855

Ala Val Lys Tyr Lys Gly His Trp Asp Phe Met Thr Asp Val Ala Asn
      1860   1865   1870

Arg Arg Asn Arg Phe Ser Glu Val Lys Glu Asn Ser Gln Ala Gly Trp
    1875   1880   1885

Tyr Tyr Gly Ala Ser Ser Lys Asp Glu Tyr Asn Arg Leu Leu Thr Lys
    1890   1895   1900

Glu Asp Ser Ala Pro Asp Gly His Ser Gly Glu Tyr Gly His Ser Ser
1905   1910   1915   1920

Glu Phe Thr Val Asn Phe Lys Glu Lys Lys Leu Thr Gly Lys Leu Phe
          1925   1930   1935

Ser Asn Leu Gln Asp Arg His Lys Gly Asn Val Thr Lys Thr Glu Arg
          1940   1945   1950

Tyr Asp Ile Asp Ala Asn Ile His Gly Asn Arg Phe Arg Gly Ser Ala
          1955   1960   1965

Thr Ala Ser Asn Lys Asn Asp Thr Ser Lys His Pro Phe Thr Ser Asp
          1970   1975   1980

Ala Asn Asn Arg Leu Glu Gly Gly Phe Tyr Gly Pro Lys Gly Glu Glu
1985   1990   1995   2000

Leu Ala Gly Lys Phe Leu Thr Asn Asp Asn Lys Leu Phe Gly Val Phe
          2005   2010   2015

Gly Ala Lys Arg Glu Ser Lys Ala Glu Glu Lys Thr Glu Ala Ile Leu
          2020   2025   2030

Asp Ala Tyr Ala Leu Gly Thr Phe Asn Thr Ser Asn Ala Thr Thr Phe
          2035   2040   2045

Thr Pro Phe Thr Glu Lys Gln Leu Asp Asn Phe Gly Asn Ala Lys Lys
          2050   2055   2060

Leu Val Leu Gly Ser Thr Val Ile Asp Leu Val Pro Thr Asp Ala Thr
2065   2070   2075   2080

Lys Asn Glu Phe Thr Lys Asp Lys Pro Glu Ser Ala Thr Asn Glu Ala
          2085   2090   2095

Gly Glu Thr Leu Met Val Asn Asp Glu Val Ser Val Lys Thr Tyr Gly
          2100   2105   2110

Lys Asn Phe Glu Tyr Leu Lys Phe Gly Glu Leu Ser Ile Gly Gly Ser
          2115   2120   2125

His Ser Val Phe Leu Gln Gly Glu Arg Thr Ala Thr Thr Gly Glu Lys
          2130   2135   2140

Ala Val Pro Thr Thr Gly Thr Ala Lys Tyr Leu Gly Asn Trp Val Gly
2145   2150   2155   2160

Tyr Ile Thr Gly Lys Asp Thr Gly Thr Gly Thr Gly Lys Ser Phe Thr
          2165   2170   2175

Asp Ala Gln Asp Val Ala Asp Phe Asp Ile Asp Phe Gly Asn Lys Ser
          2180   2185   2190

Val Ser Gly Lys Leu Ile Thr Lys Gly Arg Gln Asp Pro Val Phe Ser
          2195   2200   2205

Ile Thr Gly Gln Ile Ala Gly Asn Gly Trp Thr Gly Thr Ala Ser Thr
          2210   2215   2220

Thr Lys Ala Asp Ala Gly Gly Tyr Lys Ile Asp Ser Ser Ser Thr Gly
2225   2230   2235   2240

Lys Ser Ile Ala Ile Lys Asp Ala Asn Val Thr Gly Gly Phe Tyr Gly
                  2245   2250   2255

Pro Asn Ala Asn Glu Met Gly Gly Ser Phe Thr His Asn Ala Asp Asp
              2260   2265   2270

Ser Lys Ala Ser Val Val Phe Gly Thr Lys Arg Gln Gln Glu Val Lys
        2275   2280   2285

<210> 12
<211> 1074
<212> PRT
<213> Moraxella catarrhalis

<400> 12
Met Asn Gln Ser Lys Gln Asn Asn Lys Ser Lys Lys Ser Lys Gln Val
  1   5   10   15

Leu Lys Leu Ser Ala Leu Ser Leu Gly Leu Leu Asn Ile Thr Gln Val
              20   25   30

Ala Leu Ala Asn Thr Thr Ala Asp Lys Ala Glu Ala Thr Asp Lys Thr
          35   40   45

Asn Leu Val Val Val Leu Asp Glu Thr Val Val Thr Ala Lys Lys Asn
      50   55   60

Ala Arg Lys Ala Asn Glu Val Thr Gly Leu Gly Lys Val Val Lys Thr
 65   70   75   80

Ala Glu Thr Ile Asn Lys Glu Gln Val Leu Asn Ile Arg Asp Leu Thr
              85   90   95

Arg Tyr Asp Pro Gly Ile Ala Val Val Glu Gln Gly Arg Gly Ala Ser
              100   105   110

Ser Gly Tyr Ser Ile Arg Gly Met Asp Lys Asn Arg Val Ala Val Leu
          115   120   125

Val Asp Gly Ile Asn Gln Ala Gln His Tyr Ala Leu Gln Gly Pro Val
      130   135   140

Ala Gly Lys Asn Tyr Ala Ala Gly Gly Ala Ile Asn Glu Ile Glu Tyr
145   150   155   160

Glu Asn Val Arg Ser Val Glu Ile Ser Lys Gly Ala Asn Ser Ser Glu
              165   170   175

Tyr Gly Ser Gly Ala Leu Ser Gly Ser Val Ala Phe Val Thr Lys Thr
          180   185   190

Ala Asp Asp Ile Ile Lys Asp Gly Lys Asp Trp Gly Val Gln Thr Lys
          195   200   205

```
Thr Ala Tyr Ala Ser Lys Asn Asn Ala Trp Val Asn Ser Val Ala Ala
    210             215             220
```

```
Ala Gly Lys Ala Gly Ser Phe Ser Gly Leu Ile Ile Tyr Thr Asp Arg
225             230             235             240
```

```
Arg Gly Gln Glu Tyr Lys Ala His Asp Asp Ala Tyr Gln Gly Ser Gln
            245             250             255
```

```
Ser Phe Asp Arg Ala Val Ala Thr Thr Asp Pro Asn Asn Arg Thr Phe
            260             265             270
```

```
Leu Ile Ala Asn Glu Cys Ala Asn Gly Asn Tyr Glu Ala Cys Ala Ala
            275             280             285
```

```
Gly Gly Gln Thr Lys Leu Gln Ala Lys Pro Thr Asn Val Arg Asp Lys
    290             295             300
```

```
Val Asn Val Lys Asp Tyr Thr Gly Pro Asn Arg Leu Ile Pro Asn Pro
305             310             315             320
```

```
Leu Thr Gln Asp Ser Lys Ser Leu Leu Leu Arg Pro Gly Tyr Gln Leu
            325             330             335
```

```
Asn Asp Lys His Tyr Val Gly Gly Val Tyr Glu Ile Thr Lys Gln Asn
            340             345             350
```

```
Tyr Ala Met Gln Asp Lys Thr Val Pro Ala Tyr Leu Ala Val His Asp
    355             360             365
```

```
Ile Glu Lys Ser Arg Leu Ser Asn His Ala Gln Ala Asn Gly Tyr Tyr
    370             375             380
```

```
Gln Gly Asn Asn Leu Gly Glu Arg Ile Arg Asp Thr Ile Gly Pro Asp
385             390             395             400
```

```
Ser Gly Tyr Gly Ile Asn Tyr Ala His Gly Val Phe Tyr Asp Glu Lys
            405             410             415
```

```
His Gln Lys Asp Arg Leu Gly Leu Glu Tyr Val Tyr Asp Ser Lys Gly
            420             425             430
```

```
Glu Asn Lys Trp Phe Asp Asp Val Arg Val Ser Tyr Asp Lys Gln Asp
    435             440             445
```

```
Ile Thr Leu Arg Ser Gln Leu Thr Asn Thr His Cys Ser Thr Tyr Pro
    450             455             460
```

```
His Ile Asp Lys Asn Cys Thr Pro Asp Val Asn Lys Pro Phe Ser Val
465             470             475             480
```

```
Lys Glu Val Asp Asn Asn Ala Tyr Lys Glu Gln His Asn Leu Ile Lys
            485             490             495
```

```
Ala Val Phe Asn Lys Lys Met Ala Leu Gly Ser Thr His His His Ile
            500             505             510
```

```
Asn Leu Gln Val Gly Tyr Asp Lys Phe Asn Ser Ser Leu Ser Arg Val
            515             520             525
```

Glu Tyr Arg Leu Ala Thr His Gln Ser Tyr Gln Lys Leu Asp Tyr Thr
    530   535   540

Pro Pro Ser Asn Pro Leu Pro Asp Lys Phe Lys Pro Ile Leu Gly Ser
545   550   555   560

Asn Asn Lys Pro Ile Cys Leu Asp Ala Tyr Gly Tyr Gly His Asp His
            565   570   575

Pro Gln Ala Cys Asn Ala Lys Asn Ser Thr Tyr Gln Asn Phe Ala Ile
            580   585   590

Lys Lys Gly Ile Glu Gln Tyr Asn Gln Lys Thr Asn Thr Asp Lys Ile
            595   600   605

Asp Tyr Gln Ala Ile Ile Asp Gln Tyr Asp Lys Gln Asn Pro Asn Ser
    610   615   620

Thr Leu Lys Pro Phe Glu Lys Ile Lys Gln Ser Leu Gly Gln Glu Lys
625   630   635   640

Tyr Asn Lys Ile Asp Glu Leu Gly Phe Lys Ala Tyr Lys Asp Leu Arg
            645   650   655

Asn Glu Trp Ala Gly Trp Thr Asn Asp Asn Ser Gln Gln Asn Ala Asn
            660   665   670

Lys Gly Thr Asp Asn Ile Tyr Gln Pro Asn Gln Ala Thr Val Val Lys
            675   680   685

Asp Asp Lys Cys Lys Tyr Ser Glu Thr Asn Ser Tyr Ala Asp Cys Ser
    690   695   700

Thr Thr Arg His Ile Ser Gly Asp Asn Tyr Phe Ile Ala Leu Lys Asp
705   710   715   720

Asn Met Thr Ile Asn Lys Tyr Val Asp Leu Gly Leu Gly Ala Arg Tyr
            725   730   735

Asp Arg Ile Lys His Lys Ser Asp Val Pro Leu Val Asp Asn Ser Ala
            740   745   750

Ser Asn Gln Leu Ser Trp Asn Phe Gly Val Val Val Lys Pro Thr Asn
            755   760   765

Trp Leu Asp Ile Ala Tyr Arg Ser Ser Gln Gly Phe Arg Met Pro Ser
    770   775   780

Phe Ser Glu Met Tyr Gly Glu Arg Phe Gly Val Thr Ile Gly Lys Gly
785   790   795   800

Thr Gln His Gly Cys Lys Gly Leu Tyr Tyr Ile Cys Gln Gln Thr Val
            805   810   815

His Gln Thr Lys Leu Lys Pro Glu Lys Ser Phe Asn Gln Glu Ile Gly
    820   825   830

Ala Thr Leu His Asn His Leu Gly Ser Leu Glu Val Ser Tyr Phe Lys
        835   840   845

Asn Arg Tyr Thr Asp Leu Ile Val Gly Lys Ser Glu Glu Ile Arg Thr
    850   855   860

Leu Thr Gln Gly Asp Asn Ala Gly Lys Gln Arg Gly Lys Gly Asp Leu
865   870   875   880

Gly Phe His Asn Gly Gln Asp Ala Asp Leu Thr Gly Ile Asn Ile Leu
                885   890   895

Gly Arg Leu Asp Leu Asn Ala Ala Asn Ser Arg Leu Pro Tyr Gly Leu
            900   905   910

Tyr Ser Thr Leu Ala Tyr Asn Lys Val Asp Val Lys Gly Lys Thr Leu
        915   920   925

Asn Pro Thr Leu Ala Gly Thr Asn Ile Leu Phe Asp Ala Ile Gln Pro
    930   935   940

Ser Arg Tyr Val Val Gly Leu Gly Tyr Asp Ala Pro Ser Gln Lys Trp
945   950   955   960

Gly Ala Asn Ala Ile Phe Thr His Ser Asp Ala Lys Asn Pro Ser Glu
                965   970   975

Leu Leu Ala Asp Lys Asn Leu Gly Asn Gly Asn Ile Gln Thr Lys Gln
            980   985   990

Ala Thr Lys Ala Lys Ser Thr Pro Trp Gln Thr Leu Asp Leu Ser Gly
        995   1000   1005

Tyr Val Asn Ile Lys Asp Asn Phe Thr Leu Arg Ala Gly Val Tyr Asn
    1010   1015   1020

Val Phe Asn Thr Tyr Tyr Thr Thr Trp Glu Ala Leu Arg Gln Thr Ala
1025   1030   1035   1040

Lys Gly Ala Val Asn Gln His Thr Gly Leu Ser Gln Asp Lys His Tyr
            1045   1050   1055

Gly Arg Tyr Ala Ala Pro Gly Arg Asn Tyr Gln Leu Ala Leu Glu Met
        1060   1065   1070

Lys Phe

<210> 13
<211> 1539
<212> DNA
<213> Moraxella catarrhalis

<400> 13
atgctcgctt ttttgatagg agctgtcatg acaatcacgc ctgtttatac cacattcacc 60
cccaccaaaa cacccataaa attttttatg gctggcttga cttttctaat cgctcatatc 120
agccatgccg atgatggtcg caccgacaat caagagctaa tcaatcaaga aatagccacc 180

```
cttgaaccca tcattaacca tgctcagcct gagttattgt cccatgatgc attaacacca 240
aaaatagaac caatactggc acaaacacca aatcctgccg aagatacgct catcgccgat 300
gaggcgttac tgcttgataa ccctgatttg ctcaatcacg ccctaaattc tgctgtcatg 360
accaatcata tggcaggcgt tcacgcatta ttgcccattt atcaaaaact gcccaaagac 420
catcaaaatg gcattttact tgggtatgcc aatgccttgg ctgctttgga taagggcaac 480
gccaaaaaag ccattgatga gctacgtcgc atcatcgcca tcatgcctga atataatgtg 540
gtgcgttttc atctggcaag ggcattattt atggacaaac aaaatgaagc cgcccttgac 600
cagtttaata aattacatgc tgacaacttg ccagaggagg tgcggcaggt tgttgggcag 660
tacagacaag cgctaaaaca acgagattca tggacatggc aagtaggcat gaatctggcc 720
aaagaagaca acatcaatca aaccccaaa aacaccacgc aaggtcaatg gacttttgac 780
aaacccattg acgccatcac cctaagctac caattggggg cggataaaaa gtggtctttg 840
cccaaagggg catatgtggg agcgaacgcc caaatctatg caaacatca tcaaaatcac 900
aaaaaatac acgaccattg gggcagactg ggggcaaatt tgggctttgc tgatgccaaa 960
aaagacctta gcattgagac ctatggtgaa aaaagatttt atgggcatga gcgttatacc 1020
gacaccattg gcatacgcat gtcggttgat tatagaatca acccaaaatt tcaaagccta 1080
aacgccatag acatatcacg cctaaccaac catcggacgc ctaggggtga cagtaataac 1140
actttataca gtacctcatt gatttattac ccaaatgcca cacgctatta tcttttgggg 1200
gcagactttt atgatgaaaa agtgccacaa gacccatctg acagttatca acgccgtggc 1260
atacgcacag cgtgggggca agaatgggcg ggtggtcttt caagccgtgc ccaaatcagc 1320
atcaacaaac gccattacca aggggcaaac ctaaccagcg gtggacaaat tcgccatgat 1380
aaacagatgc aagcgtcttt atcgctttgg cacagagaca ttcacaaatg gggcatcacg 1440
ccacggctga ccatcagcac aaacatcaat aaaagcaatg acatcaaggc aaattatcac 1500
aaaaatcaaa tgtttgttga gtttagtcgc attttttga                         1539
```

<210> 14
<211> 512
<212> PRT
<213> Moraxella catarrhalis

<400> 14

```
Met Leu Ala Phe Leu Ile Gly Ala Val Met Thr Ile Thr Pro Val Tyr
 1               5                  10                  15

Thr Thr Phe Thr Pro Thr Lys Thr Pro Ile Lys Phe Phe Met Ala Gly
            20                  25                  30

Leu Thr Phe Leu Ile Ala His Ile Ser His Ala Asp Asp Gly Arg Thr
        35                  40                  45

Asp Asn Gln Glu Leu Ile Asn Gln Glu Ile Ala Thr Leu Glu Pro Ile
    50                  55                  60

Ile Asn His Ala Gln Pro Glu Leu Leu Ser His Asp Ala Leu Thr Pro
65                  70                  75                  80

Lys Ile Glu Pro Ile Leu Ala Gln Thr Pro Asn Pro Ala Glu Asp Thr
                85                  90                  95

Leu Ile Ala Asp Glu Ala Leu Leu Leu Asp Asn Pro Asp Leu Leu Asn
            100                 105                 110

His Ala Leu Asn Ser Ala Val Met Thr Asn His Met Ala Gly Val His
        115                 120                 125

Ala Leu Leu Pro Ile Tyr Gln Lys Leu Pro Lys Asp His Gln Asn Gly
    130                 135                 140
```

Ile Leu Leu Gly Tyr Ala Asn Ala Leu Ala Ala Leu Asp Lys Gly Asn
145   150   155   160

Ala Lys Lys Ala Ile Asp Glu Leu Arg Arg Ile Ile Ala Ile Met Pro
                165   170   175

Glu Tyr Asn Val Val Arg Phe His Leu Ala Arg Ala Leu Phe Met Asp
            180   185   190

Lys Gln Asn Glu Ala Ala Leu Asp Gln Phe Asn Lys Leu His Ala Asp
        195   200   205

Asn Leu Pro Glu Glu Val Arg Gln Val Val Gly Gln Tyr Arg Gln Ala
    210   215   220

Leu Lys Gln Arg Asp Ser Trp Thr Trp Gln Val Gly Met Asn Leu Ala
225   230   235   240

Lys Glu Asp Asn Ile Asn Gln Thr Pro Lys Asn Thr Thr Gln Gly Gln
            245   250   255

Trp Thr Phe Asp Lys Pro Ile Asp Ala Ile Thr Leu Ser Tyr Gln Leu
        260   265   270

Gly Ala Asp Lys Lys Trp Ser Leu Pro Lys Gly Ala Tyr Val Gly Ala
        275   280   285

Asn Ala Gln Ile Tyr Gly Lys His His Gln Asn His Lys Lys Tyr Asn
    290   295   300

Asp His Trp Gly Arg Leu Gly Ala Asn Leu Gly Phe Ala Asp Ala Lys
305   310   315   320

Lys Asp Leu Ser Ile Glu Thr Tyr Gly Glu Lys Arg Phe Tyr Gly His
            325   330   335

Glu Arg Tyr Thr Asp Thr Ile Gly Ile Arg Met Ser Val Asp Tyr Arg
            340   345   350

Ile Asn Pro Lys Phe Gln Ser Leu Asn Ala Ile Asp Ile Ser Arg Leu
        355   360   365

Thr Asn His Arg Thr Pro Arg Ala Asp Ser Asn Asn Thr Leu Tyr Ser
    370   375   380

Thr Ser Leu Ile Tyr Tyr Pro Asn Ala Thr Arg Tyr Tyr Leu Leu Gly
385   390   395   400

Ala Asp Phe Tyr Asp Glu Lys Val Pro Gln Asp Pro Ser Asp Ser Tyr
            405   410   415

Gln Arg Arg Gly Ile Arg Thr Ala Trp Gly Gln Glu Trp Ala Gly Gly
        420   425   430

Leu Ser Ser Arg Ala Gln Ile Ser Ile Asn Lys Arg His Tyr Gln Gly
        435   440   445

Ala Asn Leu Thr Ser Gly Gly Gln Ile Arg His Asp Lys Gln Met Gln
    450   455   460

Ala Ser Leu Ser Leu Trp His Arg Asp Ile His Lys Trp Gly Ile Thr
465   470   475   480

Pro Arg Leu Thr Ile Ser Thr Asn Ile Asn Lys Ser Asn Asp Ile Lys
             485   490   495

Ala Asn Tyr His Lys Asn Gln Met Phe Val Glu Phe Ser Arg Ile Phe
             500   505   510

<210> 15
<211> 2109
<212> DNA
<213> Moraxella catarrhalis

<400> 15
atgaaacaca ttcctttaac cacactgtgt gtggcaatct ctgccgtctt attaaccgct 60
tgtggtggca gtggtggttc aaatccacct gctcctacgc ccattccaaa tgctagcggt 120
tcaggtaata ctggcaacac tggtaatgct ggcggtactg ataatacagc caatgcaggt 180
aatacaggcg gtacaaactc tggtacaggc agtgccaaca caccagagcc aaaatatcaa 240
gatgtaccaa ctgagaaaaa tgaaaaagat aaagtttcat ccattcaaga acctgccatg 300
ggttatggca tggctttgag taaaattaat ctacacaacc gacaagacac gccattagat 360
gaaaaaaata tcattacctt agacggtaaa aaacaagttg cagaaggtaa aaaatcgcca 420
ttgccatttt cgttagatgt agaaaataaa ttgcttgatg ctatatagc aaaaatgaat 480
gtagcggata aaaatgccat tggtgacaga attaagaaag gtaataaaga aatctccgat 540
gaagaacttg ccaaacaaat caaagaagct gtgcgtaaaa gccatgagtt tcagcaagta 600
ttatcatcac tggaaaacaa aattttcat tcaaatgacg gaacaaccaa agcaaccaca 660
cgagatttaa aatatgttga ttatggttac tacttggcga atgatggcaa ttatctaacc 720
gtcaaaacag acaaactttg gaatttaggc cctgtgggtg tgtgtttta taatggcaca 780
acgaccgcca aagagttgcc cacacaagat gcggtcaaat ataaaggaca ttgggacttt 840
atgaccgatg ttgccaacag aagaaaccga tttagcgaag tgaaagaaaa ctctcaagca 900
ggctggtatt atggagcatc ttcaaaagat gaatacaacc gcttattaac taaagaagac 960
tctgcccctg atggtcatag cggtgaatat ggccatagca gtgagtttac tgttaatttt 1020
aaggaaaaaa aattaacagg taagctgttt agtaacctac aagaccgcca taagggcaat 1080
gttacaaaaa ccgaacgcta tgacatcgat gccaatatcc acggcaaccg cttccgtggc 1140
agtgccaccg caagcaataa aaatgacaca agcaaacacc cctttaccag tgatgccaac 1200
aataggctag aaggtggttt ttatgggcca aaaggcgagg agctggcagg taaattctta 1260
accaatgaca caaactcttt ggcgtctttt ggtgctaaac gagagagtaa agctgaggaa 1320
aaaaccgaag ccatcttaga tgcctatgca cttgggacat ttaatacaag taacgcaacc 1380
acattcaccc catttaccga aaaacaactg ataactttg gcaatgccaa aaaattggtc 1440
ttaggttcta ccgtcattga tttggtgcct actgatgcca ccaaaaatga attcaccaaa 1500
gacaagccag agtctgccac aaacgaagcg ggcgagactt gatggtgaa tgatgaagtt 1560
agcgtcaaaa cctatggcaa aaactttgaa tacctaaaat ttggtgagct tagtatcggt 1620
ggtagccata gcgtcttttt acaaggcgaa cgcaccgcta ccacaggcga gaaagccgta 1680
ccaaccacag gcacagccaa atatttgggg aactgggtag gatacatcac aggaaaggac 1740
acaggaacgg gcacaggaaa aagctttacc gatgcccaag atgttgctga ttttgacatt 1800
gattttggaa ataaatcagt cagcggtaaa cttatcacca aaggccgcca agaccctgta 1860
tttagcatca caggtcaaat cgcaggcaat ggctggacag ggacagccag caccaccaaa 1920
gcggacgcag gaggctacaa gatagattct agcagtacag caaatccat cgccatcaaa 1980
gatgccaatg ttacagggg cttttatggt ccaaatgcaa acgagatggg cgggtcattt 2040
acacacaacg ccgatgacag caaagcctct gtggtctttg cacaaaaag acaacaagaa 2100
gttaagtag 2109

<210> 16
<211> 512
<212> PRT
<213> Moraxella catarrhalis

<400> 16

```
Met Leu Ala Phe Leu Ile Gly Ala Val Met Thr Ile Thr Pro Val Tyr
 1               5                  10                  15

Thr Thr Phe Thr Pro Thr Lys Thr Pro Ile Lys Phe Phe Met Ala Gly
            20              25                  30

Leu Thr Phe Leu Ile Ala His Ile Ser His Ala Asp Asp Gly Arg Thr
            35                  40                  45

Asp Asn Gln Glu Leu Ile Asn Gln Glu Ile Ala Thr Leu Glu Pro Ile
    50                  55                  60

Ile Asn His Ala Gln Pro Glu Leu Leu Ser His Asp Ala Leu Thr Pro
65                  70                  75                  80

Lys Ile Glu Pro Ile Leu Ala Gln Thr Pro Asn Pro Ala Glu Asp Thr
            85                  90                  95

Leu Ile Ala Asp Glu Ala Leu Leu Leu Asp Asn Pro Asp Leu Leu Asn
            100             105             110

His Ala Leu Asn Ser Ala Val Met Thr Asn Asn Met Ala Gly Val His
        115             120             125

Ala Leu Leu Pro Ile Tyr Gln Lys Leu Pro Lys Asp His Gln Asn Gly
    130             135             140

Ile Leu Leu Gly Tyr Ala Asn Ala Leu Val Ala Leu Asp Lys Gly Asn
145             150             155             160

Ala Lys Ala Ala Ile Gly Glu Leu Arg Arg Ile Ile Ala Ile Met Pro
            165             170             175

Glu Tyr Asn Val Val Arg Phe His Leu Ala Arg Ala Leu Phe Met Asp
        180             185             190

Lys Gln Asn Glu Ala Ala Leu Asp Gln Phe Asn Lys Leu His Ala Asp
    195             200             205

Asn Leu Pro Glu Glu Val Arg Arg Val Val Gly Gln Tyr Arg Gln Ala
    210             215             220

Leu Lys Gln Arg Asp Ser Trp Thr Trp Gln Val Gly Met Asn Leu Ala
225             230             235             240

Lys Glu Asp Asn Ile Asn Gln Thr Pro Lys Asn Thr Thr Gln Gly Gln
            245             250             255

Trp Thr Phe Asp Lys Pro Ile Asp Ala Ile Thr Leu Ser Tyr Gln Leu
            260             265             270

Gly Ala Asp Lys Lys Trp Ser Leu Pro Lys Gly Ala Tyr Val Gly Ala
            275             280             285

Asn Ala Gln Ile Tyr Gly Lys His His Gln Asn His Lys Lys Tyr Asn
    290             295             300
```

Asp His Trp Gly Arg Leu Gly Ala Asn Leu Gly Phe Ala Asp Ala Lys
305   310   315   320

Lys Asp Leu Ser Ile Glu Thr Tyr Gly Glu Lys Arg Phe Tyr Gly His
                325   330   335

Glu Arg Tyr Thr Asp Thr Ile Gly Ile Arg Met Ser Ala Asp Tyr Arg
            340   345   350

Ile Asn Pro Lys Phe Gln Ser Leu Asn Ala Ile Asp Ile Ser Arg Leu
            355   360   365

Thr Asn His Arg Thr Pro Arg Ala Asp Ser Asn Asn Thr Leu Tyr Ser
    370   375   380

Thr Ser Leu Ile Tyr Tyr Pro Asn Ala Thr Arg Tyr Tyr Leu Leu Gly
385   390   395   400

Ala Asp Phe Tyr Asp Glu Lys Val Pro Gln Asp Pro Ser Asp Ser Tyr
            405   410   415

Glu Arg Arg Gly Ile Arg Thr Ala Trp Gly Gln Glu Trp Ala Gly Gly
            420   425   430

Leu Ser Ser Arg Ala Gln Ile Ser Ile Asn Lys Arg His Tyr Gln Gly
            435   440   445

Ala Asn Leu Thr Ser Gly Gly Gln Ile Arg Gln Asp Lys Gln Met Gln
    450   455   460

Ala Ser Leu Ser Leu Trp His Arg Asp Ile His Lys Trp Gly Ile Thr
465   470   475   480

Pro Arg Leu Thr Ile Ser Thr Asn Ile Asn Lys Ser Asn Asp Ile Lys
            485   490   495

Ala Asn Tyr His Lys Asn Gln Met Phe Val Glu Phe Ser Arg Ile Phe
            500   505   510

<210> 17
<211> 10
<212> PRT
<213> Moraxella catarrhalis

<400> 17
Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly
  1   5   10

<210> 18
<211> 30
<212> DNA
<213> Moraxella catarrhalis

<400> 18
attcgagact taacacgcta tgaccctggc   30

<210> 19
<211> 30
<212> DNA
<213> Moraxella catarrhalis

<400> 19
attcgtgatt taactcgcta tgaccctggt   30

<210> 20
<211> 23
<212> DNA
<213> Moraxella catarrhalis

<400> 20
gatgggataa gcacgcccta ctt   23

<210> 21
<211> 25
<212> DNA
<213> Moraxella catarrhalis

<400> 21
cccatcagcc aaacaaacat tgtgt   25

<210> 22
<211> 7
<212> PRT
<213> Moraxella catarrhalis

<400> 22
Leu Glu Gly Gly Phe Tyr Gly
  1   5